

JG10 Rec'd PCT/PTO 22 MAR 2002

**TRANSMITTAL LETTER TO THE UNITED STATES  
DESIGNATED/ELECTED OFFICE (DO/EO/US)  
CONCERNING A FILING UNDER 35 U.S.C. 371**

ATTORNEY'S DOCKET NUMBER

01975 0034

U.S. APPLICATION NO  
(If known, see 37CFR1.5)**10/088744**

INTERNATIONAL APPLICATION NO.

PCT/EP00/09584

INTERNATIONAL FILING DATE

September 25, 2000

PRIORITY DATE CLAIMED

September 24, 1999

TITLE OF INVENTION

**HUMAN G-PROTEIN COUPLED RECEPTOR**

APPLICANT(S) FOR DO/EO/US

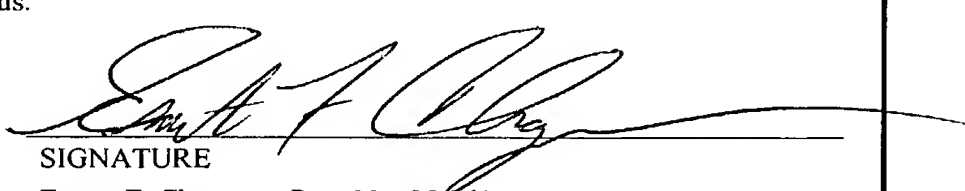
**Willy DELEERSNIJDER; Guy NYS; Jakob VENEMA; Claudia BERGER; Christiane LÖKEN**

Applicant(s) herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☐ This is an express request to begin national examination procedures (35 U.S.C. 371(f)). The submission must include items (5), (6), (9) and (21) indicated below.
4. ☒ The US has been elected by the expiration of 19 months from the priority date (Article 31).
5. ☒ A copy of the International Application as filed (35 U.S.C. 371 (c)(2)).
  - a. ☒ is attached hereto (required only if not communicated by the International Bureau)
  - b. ☐ has been communicated by the International Bureau.
  - c. ☐ is not required, as the application was filed with the United States Receiving Office (RO/US).
6. ☐ An English language translation of the International Application as filed (35 U.S.C. 371 (c)(2))
  - a. ☐ is attached hereto.
  - b. ☐ has been previously submitted under 35 U.S.C. 154 (d)(4).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371 (c)(3)).
  - a. ☐ are attached hereto (required only if not communicated by the International Bureau).
  - b. ☐ have been communicated by the International Bureau.
  - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
  - d. ☒ have not been made and will not be made.
8. ☐ An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371 (c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371 (c)(4)).
10. ☒ Annexes of the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371 (c)(5)).

Items 11 to 20 below concern document(s) or information included:

11. ☒ Information Disclosure Statement under 37 CFR 1.97 and 1.98
12. ☒ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☒ A **FIRST** preliminary amendment.
14. ☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
15. ☐ A Substitute specification.
16. ☐ A change of power of attorney and/or address letter.
17. ☐ A computer-readable form of the sequence listing in accordance with PCT Rule 13ter.2 and 35 U.S.C. 1.821-1.825.
18. ☐ A second copy of the published international application under 35 U.S.C. 154 (d)(4).
19. ☐ A second copy of the English language translation of the international application 35 U.S.C. 154 (d)(4).
20. ☒ Other items or information:
  - a. ☒ Copy of cover page of International Publication No. WO01/25269A2
  - b. ☐ Copy of Notification of Missing Requirements.
  - c. ☒ Sequence Listing - 28 pages

U.S. APPLICATION NO. (If known, see 37CFR 1.5) <b>10/088744</b>		INTERNATIONAL APPLICATION NO. PCT/EP00/09584		ATTORNEY'S DOCKET NUMBER 01975.0034																																			
21. <input checked="" type="checkbox"/> The following fees are submitted:				CALCULATIONS PTO USE ONLY																																			
<b>BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)):</b>  Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO ..... <b>\$1040.00</b>  International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO ..... <b>\$890.00</b>  International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search fee (37 CFR 1.445(a)(2)) paid to USPTO ..... <b>\$740.00</b>  International preliminary examination fee (37 CFR 1.482) paid to USPTO but all claims did not satisfy provisions of PCT Article 33(1)-(4) ..... <b>\$710.00</b>  International preliminary examination fee (37 CFR 1.482) paid to USPTO and all claims satisfied provisions of PCT Article 33 (1)-(4) ..... <b>\$100.00</b>  <div style="text-align: right;"><b>ENTER APPROPRIATE BASIC FEE AMOUNT =</b></div>																																							
						Surcharge of \$130.00 for furnishing the oath or declaration later than months from the earliest claimed priority date (37 CFR 1.492 (e)). <input type="checkbox"/> 20 <input type="checkbox"/> 30		\$																															
						<table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="width: 15%;">CLAIMS</th> <th style="width: 15%;">NUMBER FILED</th> <th style="width: 15%;">NUMBER EXTRA</th> <th style="width: 15%;">RATE</th> <th style="width: 15%;"></th> <th style="width: 15%;"></th> </tr> </thead> <tbody> <tr> <td>Total Claims</td> <td>47</td> <td>- 20 =</td> <td>27</td> <td>x \$18.00</td> <td>\$486.00</td> </tr> <tr> <td>Independent Claims</td> <td>9</td> <td>-3 =</td> <td>6</td> <td>x \$84.00</td> <td>\$504.00</td> </tr> <tr> <td colspan="4">MULTIPLE DEPENDENT CLAIM(S) (if applicable)</td> <td>+\$280.00</td> <td>\$280.00</td> </tr> <tr> <td colspan="5" style="text-align: right;"><b>TOTAL OF THE ABOVE CALCULATIONS =</b></td> <td>\$2160.00</td> </tr> </tbody> </table>		CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE			Total Claims	47	- 20 =	27	x \$18.00	\$486.00	Independent Claims	9	-3 =	6	x \$84.00	\$504.00	MULTIPLE DEPENDENT CLAIM(S) (if applicable)				+\$280.00	\$280.00	<b>TOTAL OF THE ABOVE CALCULATIONS =</b>					\$2160.00		
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<b>TOTAL NATIONAL FEE =</b>		2160.00																																					
Fee for recording the enclosed assignment (37 CFR 1.21 (h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). <b>\$40.00</b> per property.		+\$40.00																																					
<b>TOTAL FEES ENCLOSED =</b>		\$2200.00																																					
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				charged:	\$																																		
a. <input checked="" type="checkbox"/> A check in the amount of \$ <u>2200.00</u> to cover the above fees is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. _____ in the amount of \$ _____ to cover the above fees. A duplicate copy of this sheet is enclosed. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>06-0916</u> . A duplicate copy of this sheet is enclosed. d. <input type="checkbox"/> Fees are to be charged to a credit card. <b>WARNING:</b> Information on this form may become public. <b>Credit card information should not be included on this form.</b> Provide credit card information and authorization on PTO-2038.																																							
NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137 (a) or (b)) must be filed and granted to restore the application to pending status.																																							
<b>SEND ALL CORRESPONDENCE TO:</b> Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P. 1300 I Street, N.W. Washington, D.C. 20005-3315																																							
DATED: March 22, 2002				<div style="text-align: center;">             SIGNATURE            Ernest F. Chapman, Reg. No. 25,961            NAME/REGISTRATION NO.         </div>																																			

Customer No. 22,852  
Attorney Docket No. 01975.0034

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re Application of: )  
)  
Willy DELEERSNIJDER et al. )  
) Group Art Unit:  
Serial No.: Not Yet Assigned )  
) Examiner:  
Filed: March 22, 2002 )  
)  
For: HUMAN G-PROTEIN )  
COUPLED RECEPTOR )

U.S. NATIONAL PHASE OF PCT/EP00/09584

**Assistant Commissioner for Patents**  
**Washington, DC 20231**

**BOX: PCT**

Sir:

**PRELIMINARY AMENDMENT**

Prior to examination, please amend the above-identified application as follows:

**IN THE SPECIFICATION:**

Please amend the specification as follows:

Page 1, after the title, insert the following new heading and paragraph:

**CROSS REFERENCE TO RELATED APPLICATIONS**

The application claims the benefit of U.S. Provisional Application No. 60/222,047, filed July 31, 2000, the content of which is incorporated herein by reference, and claims the right to priority based on European Patent Application No. 99203140.1, filed September 24, 1999, Netherlands Patent Application No. 1013140, filed September 24, 1999, and European Patent Application No. 00202683.9, filed July 28, 2000.

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**REMARKS**


The examiner is respectfully requested to consider the above preliminary amendment prior to examination of the application. No new matter has been introduced by these amendments.

If there are any fees due in connection with the filing of this amendment, please charge the fees to Deposit Account No. 06-0916. If a fee is required for an extension of time under 37 C.F.R. § 1.136 not accounted for above, such an extension is requested and the fee should also be charged to our deposit account.

Respectfully submitted,

FINNEGAN, HENDERSON, FARABOW,  
GARRETT & DUNNER, L.L.P.

Dated: March 22, 2002

By   
Ernest F. Chapman  
Reg. No. 25,961

EFC/FPD/peg

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10/088744  
Rec'd PCT/PTO 22 JUL 2002

Attorney Docket No. 01975.0034  
Customer Number 22,852

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re U.S. National Phase Application of:  
PCT/EP00/09584

)  
)  
) Group Art Unit:

Inventors: Willy DELEERSNIJDER et al.

)  
) Examiner:

Serial No.: 10/088,744

Filed: March 22, 2002

For: HUMAN G-PROTEIN COUPLED  
RECEPTOR

Assistant Commissioner for Patents  
Washington, DC 20231

Sir:

STATEMENT

The information recorded in computer readable form (attached diskette) is  
identical to the written sequence listing.

Respectfully submitted,

FINNEGAN, HENDERSON, FARABOW,  
GARRETT & DUNNER, L.L.P.

Dated: July 22, 2002

By: 

Ernest F. Chapman  
Reg. No. 25,961

EFC/FPD/peg  
Enclosures

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Novel human G-protein coupled receptor**Description**

5 The present invention relates to novel identified polynucleotides, polypeptides encoded by them and to the use of such polynucleotides and polypeptides, and to their production. More particularly, the polynucleotides and polypeptides of the present invention relate to a G-protein coupled receptor (GPCR), hereinafter referred to as IGS4. IGS4 exists in two polymorphic forms, hereinafter referred to as IGS4A and IGS4B. The invention also relates to inhibiting or activating the action of such  
10 polynucleotides and polypeptides, to a vector containing said polynucleotides, a host cell containing such vector and transgenic animals where the IGS4-gene is either overexpressed, misexpressed, underexpressed and/or suppressed (knock-out animals). The invention further relates to a method for screening compounds capable to act as an agonist or an antagonist of said G-protein coupled receptor IGS4, and to the cognate ligand of IGS4.

**BACKGROUND OF THE INVENTION**

It is well established that many medically significant biological processes are mediated by proteins participating in signal transduction pathways that involve G-proteins and/or second messengers; e.g.,  
20 cAMP (Lefkowitz, Nature, 1991, 351:353-354). Herein these proteins are referred to as proteins participating in pathways with G-proteins. Some examples of these proteins include the GPC receptors; such as those for adrenergic agents and dopamine (Kobilka, B.K., et al., Proc. Natl. Acad. Sci., USA, 1987, 84:46-50; Kobilka, B.K., et al., Science, 1987, 238:650-656; Bunzow, J.R., et al., Nature, 1988, 336:783-787), G-proteins themselves, effector proteins, e.g., phospholipase C, adenylate cyclase, and  
25 phosphodiesterase, and actuator proteins, e.g., protein kinase A and protein kinase C (Simon, M.I., et al., Science, 1991, 252:802-8).

For example, in one form of signal transduction, upon hormone binding to a GPCR the receptor interacts with the heterotrimeric G-protein and induces the dissociation of GDP from the guanine  
30 nucleotide-binding site. At normal cellular concentrations of guanine nucleotides, GTP fills the site immediately. Binding of GTP to the  $\alpha$  subunit of the G-protein causes the dissociation of the G-protein from the receptor and the dissociation of the G-protein into  $\alpha$  and  $\beta\gamma$  subunits. The GTP-carrying form then binds to activated adenylate cyclase. Hydrolysis of GTP to GDP, catalyzed by the G-protein itself ( $\alpha$  subunit possesses an intrinsic GTPase activity), returns the G-protein to its basal, inactive form. The  
35 GTPase activity of the  $\alpha$  subunit is, in essence, an internal clock that controls an on/off switch. The GDP bound form of the  $\alpha$  subunit has high affinity for  $\beta\gamma$  and subsequent reassociation of  $\alpha$ GDP with  $\beta\gamma$  returns the system to the basal state. Thus the G-protein serves a dual role, as an intermediate that relays the signal from receptor to effector (in this example adenylate cyclase), and as a clock that controls the duration of the signal.

The membrane bound superfamily of G-protein coupled receptors has been characterized as having seven putative transmembrane domains. The domains are believed to represent transmembrane  $\alpha$ -helices connected by extracellular or cytoplasmic loops. G-protein coupled receptors include a wide  
5 range of biologically active receptors, such as hormone, viral, growth factor and neuroreceptors.

The G-protein coupled receptor family includes dopamine receptors which bind to neuroleptic drugs used for treating CNS disorders. Other examples of members of this family include, but are not limited to calcitonin, adrenergic, neuropeptideY, somastotatin, neurotensin, neurokinin, capsaicin, VIP,  
10 CGRP, CRF, CCK, bradykinin, galanin, motilin, nociceptin, endothelin, cAMP, adenosine, muscarinic, acetylcholine, serotonin, histamine, thrombin, kinin, follicle stimulating hormone, opsin, endothelial differentiation gene-1, rhodopsin, odorant, and cytomegalovirus receptors.

Most G-protein coupled receptors have single conserved cysteine residues in each of the first two  
15 extracellular loops which form disulfide bonds that are believed to stabilize functional protein structures. The 7 transmembrane regions are designated as TM1, TM2, TM3, TM4, TM5, TM6 and TM7. The cytoplasmic loop which connects TM5 and TM6 may be a major component of the G-protein binding domain.

Most G-protein coupled receptors contain potential phosphorylation sites within the third  
20 cytoplasmic loop and/or the carboxy terminus. For several G-protein coupled receptors, such as the  $\beta$ -adrenoreceptor, phosphorylation by protein kinase A and/or specific receptor kinases mediates receptor desensitization.

Recently, it was discovered that certain GPCRs, like the calcitonin-receptor like receptor, might  
25 interact with small single pass membrane proteins called receptor activity modifying proteins (RAMP's). This interaction of the GPCR with a certain RAMP is determining which natural ligands have relevant affinity for the GPCR-RAMP combination and regulate the functional signaling activity of the complex (McLathie, L.M. et al., Nature (1998) 393:333-339).

For some receptors, the ligand binding sites of G-protein coupled receptors are believed to  
30 comprise hydrophilic sockets formed by several G-protein coupled receptor transmembrane domains, said sockets being surrounded by hydrophobic residues of the G-protein coupled receptors. The hydrophilic side of each G-protein coupled receptor transmembrane helix is postulated to face inward and form a polar ligand-binding site. TM3 has been implicated in several G-protein coupled receptors as  
35 having a ligand-binding site, such as the TM3 aspartate residue. TM5 serines, a TM6 asparagine and TM6 or TM7 phenylalanines or tyrosines are also implicated in ligand binding.

G-protein coupled receptors can be intracellularly coupled by heterotrimeric G-proteins to various intracellular enzymes, ion channels and transporters (see, Johnson et al., Endoc. Rev., 1989, 10:317-331). Different G-protein  $\alpha$ -subunits preferentially stimulate particular effectors to modulate various biological functions in a cell. Phosphorylation of cytoplasmic residues of G-protein coupled receptors has been identified as an important mechanism for the regulation of G-protein coupling of some G-protein coupled receptors. G-protein coupled receptors are found in numerous sites within a mammalian host.

Receptors - primarily the GPCR class - have led to more than half of the currently known drugs (Drews, Nature Biotechnology, 1996, 14: 1516). This indicates that these receptors have an established, proven history as therapeutic targets. Clearly there is a need for identification and characterization of further receptors which can play a role in preventing, ameliorating or correcting dysfunctions or diseases, including, but not limited to PNS, psychiatric and CNS disorders, including schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive disorder (OCD), post traumatic stress disorder (PTSD), phobia and panic, major depressive disorder, bipolar disorder, Parkinson's disease, general anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer disease/dementia and other neurodegenerative diseases, severe mental retardation, dyskinesias, Huntington's disease, Tourett's syndrome, tics, tremor, dystonia, spasms, anorexia, bulimia, stroke, addiction/dependency/craving, sleep disorder, epilepsy, migraine; attention deficit/hyperactivity disorder (ADHD); cardiovascular diseases, including heart failure, angina pectoris, arrhythmias, myocardial infarction, cardiac hypertrophy, hypotension, hypertension - e.g. essential hypertension, renal hypertension, or pulmonary hypertension, thrombosis, arteriosclerosis, cerebral vasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney disease - e.g. renal failure; dyslipidemias; obesity; emesis; gastrointestinal disorders, including irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), gastroesophageal reflux disease (GERD), motility disorders and conditions of delayed gastric emptying, such as post operative or diabetic gastroparesis, and diabetes, ulcers - e.g. gastric ulcer; diarrhoea; other diseases including osteoporosis; inflammations; infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; pain; cancers; chemotherapy induced injury; tumor invasion; immune disorders; urinary retention; asthma; allergies; arthritis; benign prostatic hypertrophy; endotoxin shock; sepsis; complication of diabetes mellitus; and gynaecological disorders.

#### SUMMARY OF THE INVENTION

In one aspect, the invention relates to IGS4 polypeptides (including the IGS4A and IGS4B polypeptide polymorphs), polynucleotides and recombinant materials and methods for their production. Another aspect of the invention relates to methods for using such IGS4 polypeptides, polynucleotides and recombinant materials. Such uses include, but are not limited to, use as a therapeutic target and for the treatment of PNS, psychiatric and CNS disorders, including schizophrenia, episodic paroxysmal

anxiety (EPA) disorders such as obsessive compulsive disorder (OCD), post traumatic stress disorder (PTSD), phobia and panic, major depressive disorder, bipolar disorder, Parkinson's disease, general anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer disease/dementia and other neurodegenerative diseases, severe mental retardation, dyskinesias, Huntington's disease, Tourett's syndrome, tics, tremor, dystonia, spasms, anorexia, bulimia, stroke, addiction/dependency/craving, sleep disorder, epilepsy, migraine; attention deficit/hyperactivity disorder (ADHD); cardiovascular diseases, including heart failure, angina pectoris, arrhythmias, myocardial infarction, cardiac hypertrophy, hypotension, hypertension – e.g. essential hypertension, renal hypertension, or pulmonary hypertension, thrombosis, arteriosclerosis, cerebral vasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney disease – e.g. renal failure; dyslipidemias; obesity; emesis; gastrointestinal disorders, including irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), gastroesophageal reflux disease (GERD), motility disorders and conditions of delayed gastric emptying, such as post operative or diabetic gastroparesis, and diabetes, ulcers – e.g. gastric ulcer; diarrhoea; other diseases including osteoporosis; inflammations; infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; pain; cancers; chemotherapy induced injury; tumor invasion; immune disorders; urinary retention; asthma; allergies; arthritis; benign prostatic hypertrophy; endotoxin shock; sepsis; complication of diabetes mellitus; and gynaecological disorders, among others. Preferred uses of the invention relate to disorders of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), disorders of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal muscle and/or of the thyroid, and/or also to lung diseases, immunological diseases and disorders of the genitourinary system.

In still another aspect, the invention relates to methods to identify agonists and antagonists using the materials provided by the invention, and treating conditions associated with IGS4 imbalance with the identified compounds. Yet another aspect of the invention relates to diagnostic assays for detecting diseases associated with inappropriate IGS4 activity or levels. A further aspect of the invention relates to animal-based systems which act as models for disorders arising from aberrant expression or activity of IGS4. Preferred agonists or antagonists identified according to the present invention are those which are suited for the treatment of disorders of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), disorders of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal muscle and/or of the thyroid, and/or also to lung diseases, immunological diseases and disorders of the genitourinary system.

The invention also relates to the identification of the cognate ligand of the IGS4 polypeptides of the invention. High affinity binding to said IGS4 polypeptides is found for the neuropeptides known as neuromedin U.

Table 1: IGS4A-DNA of SEQ ID NO: 1 and SEQ ID NO: 3

5' -

5 GGCTCAGCTTGAAACAGAGCCTCGTACCAGGGGAGGCTCAGGCCTTGGATTTTAATGTCA  
GGGATGGAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAACTAGAAGATCCATTC  
CAGAAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGC  
CACTTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGTCAATTGGC  
AATGTCCTGGTGTGCCTGGTGATTCTGCAGCACCGAGGCTATGAAGACGCCCACCAACTAC  
10 TACCTCTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCTGGAG  
GTCTATGAGATGTGGCGCAACTACCCTTTCTTGTTTCGGGCCCCGTGGGCTGCTACTTCAAG  
ACGGCCCTCTTTGAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTG  
GAGCGCTACGTGGCCATCCTACACCCGTTCCGCGCCAAACTGCAGAGCACCCGGCGCCGG  
GCCCTCAGGATCCTCGGCATCGTCTGGGGCTTCTCCGTGCTCTTCTCCCTGCCCAACACC  
15 AGCATCCATGGCATCAAGTTCCACTACTTCCCCAATGGGTCCCTGGTCCCAGGTTTCGGCC  
ACCTGTACGGTCATCAAGCCCATGTGGATCTACAATTTTCATCATCCAGGTCACCTCCTTC  
CTATTCTACCTCCTCCCCATGACTGTCATCAGTGTCTCTACTACCTCATGGCACTCAGA  
CTAAAGAAAGACAAATCTCTTGAGGCAGATGAAGGGAATGCAAATATTCAAAGACCCTGC  
AGAAAATCAGTCAACAAGATGCTGTTTGTCTTGGTCTTAGTGTTTGCTATCTGTTGGGCC  
20 CCGTTCCACATTGACCGACTCTTCTTCAGCTTTGTGGAGGAGTGGAGTGAATCCCTGGCT  
GCTGTGTTCAACCTCGTCCATGTGGTGTGAGGTGTCTTCTTCTACCTGAGCTCAGCTGTC  
AACCCCATTTATCTATAACCTACTGTCTCGCCGCTTCCAGGCAGCATTCCAGAATGTGATC  
TCTTCTTTCCACAAACAGTGGCACTCCCAGCATGACCCACAGTTGCCACCTGCCCAGCGG  
AACATCTTCCTGACAGAATGCCACTTTGTGGAGCTGACCGAAGATATAGGTCCCCAATTC  
25 CCATGTCAGTCATCCATGCACAACTCTCACCTCCCAACAGCCCTCTCTAGTGAACAGATG  
TCAAGAACAAACTATCAAAGCTTCCACTTTAACAAAACCTGAATTCTTTCAGAGCTGACT  
CTCCTCTATGCCTCAAACTTCAGAGAGGAACATCCCATAATGTATGCCTTCTCATATGA  
TATTAGAGAGGTAGAATGGCTCTTACAACCTCATGTACCCATTGCTAGTTTTTTTTTTTA  
ATAAACGTGAAAACCTGAGAGTTAGATCTGGTTTCAAACCCCAAGACTGCCTGATTTTTAG  
30 TTATCTTTCCACTATCCTAACTGCCTCATGCCCCCTTCACTAGTTCATGCCAAGAACGTGA  
CTGGAAAGGCATGGCACCTATACCTTGATTAATTTCCATTAATGGAAATGGTTCGTCCTG  
AGTCATCTACGTTCCGAGTCAGGCTGTCACTCCTACTA - 3'

Table 2: IGS4B-DNA of SEQ ID NO: 5 and SEQ ID NO: 7

5' -  
5 GGCTCAGCTTGAAACAGAGCCTCGTACCAGGGGAGGCTCAGGCCTTGGATTTTAATGTCA  
GGGATGGAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAACTAGAAGATCCATTC  
CAGAAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGC  
CACTTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTGTGGTGGGGGTCAATTGGC  
AATGTCCTGGTGTGCCTGGTGATTCTGCAGCACCAAGGCTATGAAGACGCCCACCAACTAC  
TACCTCTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTGCTCCTTGGGAATGCCCCTGGAG  
10 GTCTATGAGATGTGGCGCAACTACCTTTTCTTGTTTCGGGCCCCGTGGGCTGCTACTTCAAG  
ACGGCCCTCTTTGAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTG  
GAGCGCTACGTGGCCATCCTACACCCGTTCCGCGCCAAACTGCAGAGCACCCGGCGCCGG  
GCCCTCAGGATCCTCGGCATCGTCTGGGGCTTCTCCGTGCTCTTCTCCCTGCCCAACACC  
AGCATCCATGGCATCAAGTTCCTACTTCCCCAATGGGTCCCTGGTCCCAGGTTCGGCC  
15 ACCTGTACGGTCATCAAGCCCATGTGGATCTACAATTTTCATCATCCAGGTCACCTCCTTC  
CTATTCTACCTCCTCCCCATGACTGTCATCAGTGTCTCTACTACCTCATGGCACTCAGA  
CTAAAGAAAGACAAATCTCTTGAGGCAGATGAAGGGAATGCAAATATTCAAAGACCCTGC  
AGAAAATCAGTCAACAAGATGCTGTTTGTCTTGGTCTTAGTGTTTGCTATCTGTTGGGCC  
CCGTTCCACATTGACCGACTCTTCTTCAGCTTTGTGGAGGAGTGGACTGAATCCCTGGCT  
20 GCTGTGTTCAACCTCGTCCATGTGGTGTGAGGTGTCTTATTCTACCTGAGCTCAGCTGTC  
AACCCCATTTATCTATAACCTACTGTCTCGCCGCTTCCAGGCAGCATTCCAGAATGTGATC  
TCTTCTTTCCACAAACAGTGGCACTCCCAGCATGACCCACAGTTGCCACCTGCCCAGCGG  
AACATCTTCCTGACAGAATGCCACTTTGTGGAGCTGACCGAAGATATAGGTCCCCAATTC  
CTATGTCAGTCATCCGTGCACAACTCTCACCTCCCAACAGCCCTCTCTAGTGAACAGATG  
25 TCAAGAACAACTATCAAAGCTTCCACTTTAACAAAACCTGAATTCTTTCAGAGCTGACT  
CTCCTCTATGCCTCAAACTTCAGAGAGGAACATCCCATAATGTATGCCTTCTCATATGA  
AATTAGAGAGGTAGAATGGCTCTTACAACCTCATGTACCCATTGCTAGTTTTTTTTTTTA  
ATAAACGTGAAAACCTGAGAGTTAGATCTGGTTTCAAAACCCAAGACTGCCTGATTTTTAG  
TTATCTTTCCACTATCCTAACTGCCTCATGCCCCCTTCACTAGTTCATGCCAAGAACGTGA  
30 CTGGAAAGGCATGGCACCTATACCTTGATTAATTTCCATTAATGGAAATGGTTCGTCCTG  
AGTCATCTACGTTCCGAGTCAGGCTGTCACTCCTACTA-3'

Table 3: IGS4A-64-DNA of SEQ ID NO: 9 and SEQ ID NO: 11

	5' -
5	GGCTCAGCTTGAAACAGAGCCTCGTACCAGGGGAGGCTCAGGCCTTGGATTTTAATGTCA GGGATGGAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAACTAGAAGATCCATTC CAGAAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGC CACTTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTGTGGTGGGGGTCATTGGC AATGTCCTGGTGTGCCTGGTGAATCTGCAGCACCGAGCTATGAAGACGCCCACCAACTAC
10	TACCTCTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCTGGAG GTCTATGAGATGTGGCGCAACTACCCTTTCTTGTTTCGGGCCCCGTGGGCTGCTACTTCAAG ACGGCCCTCTTTGAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTG GAGCGCTACGTGGCCATCCTACACCCGTTCCGCGCCAAACTGCAGAGCACCCGGCGCCGG GCCCTCAGGATCCTCGGCATCGTCTGGGGCTTCTCCGTGCTCTTCTCCCTGCCCAACACC
15	AGCATCCATGGCATCAAGTTCCACTACTTCCCCAATGGGTCCCTGGTCCCAGGTTTCGGCC ACCTGTACGGTCATCAAGCCCATGTGGATCTACAATTTTCATCATCCAGGTCACCTCCTTC CTATTCTACCTCCTCCCCATGACTGTCATCAGTGTCTCTACTACCTCATGGCACTCAGA CTAAAGAAAGACAAATCTCTTGAGGCAGATGAAGGGAATGCAAATATTCAAAGACCCTGC AGAAAATCAGTCAACAAGATGCTGTCTTTGTGGAGGAGTGGAGTGAATCCCTGGCTGCTG
20	TGTTCAACCTCGTCCATGTGGTGTGAGGTGTCTTCTTCTACCTGAGCTCAGCTGTCAACC CCATTATCTATAACCTACTGTCTCGCCGCTTCCAGGCAGCATTCCAGAATGTGATCTCTT CTTTCCACAAACAGTGGCACTCCCAGCATGACCCACAGTTGCCACCTGCCCAGCGGAACA TCTTCCTGACAGAATGCCACTTTGTGGAGCTGACCGAAGATATAGGTCCCCAATTCCCAT GTCAGTCATCCATGCACAACCTCTCACCTCCCAACAGCCCTCTCTAGTGAACAGATGTCAA
25	GAACAAACTATCAAAGCTTCCACTTTAACAAAACCTGAATTCTTTCAGAGCTGACTCTCC TCTATGCCTCAAAACTTCAGAGAGGAACATCCCATAATGTATGCCTTCTCATATGATATT AGAGAGGTAGAATGGCTCTTACAACCTCATGTACCCATTGCTAGTTTTTTTTTTTAATAA ACGTGAAAACCTGAGAGTTAGATCTGGTTTCAAAACCCAAGACTGCCTGATTTTTTAGTTAT CTTTCCACTATCCTAACTGCCTCATGCCCCTTCACTAGTTCATGCCAAGAACGTGACTGG
30	AAAGGCATGGCACCTATACCTTGATTAATTTCCATTAATGGAAATGGTTCGTCCTGAGTC ATCTACGTTCCGAGTCAGGCTGTCACTCCTACTA-3'



**Table 4: IGS4A-protein of SEQ ID NO: 2 and SEQ ID NO: 4 (without the three amino acids between brackets).**

5 (MSG) MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGV  
 IGNVLVCLVILQHQAMKTPTNYLFS LAVSDLLVLLLGM PLEVYEMWRNYPFLFGPVGCY  
 FKTALFETVCFASILSITTVSVERYVAILHPPFRAKLQSTRRRALRILGIVWGFSVLFSLP  
 NTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMA  
 LRLKKDKSLEADEGNANIQRPCRKSVNKMLFVLVLVFAICWAPFHIDRLFFSFVEEWSSES  
 10 LAAVFNLVHVVS GVFYLLSSAVNP I IYNLLSRRFQAAFQNVISSFHKQWHSQHDPQLPPA  
 QRNIFLTECHFVELTEDIGPQFPCQSSMHNSHLPTALSSEQMSRTNYQSFHFNKT

**Table 5: IGS4B-protein of SEQ ID NO: 6 and SEQ ID NO: 8 (without the three amino acids between brackets).**

15 (MSG) MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGV  
 IGNVLVCLVILQHQAMKTPTNYLFS LAVSDLLVLLLGM PLEVYEMWRNYPFLFGPVGCY  
 FKTALFETVCFASILSITTVSVERYVAILHPPFRAKLQSTRRRALRILGIVWGFSVLFSLP  
 NTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMA  
 20 LRLKKDKSLEADEGNANIQRPCRKSVNKMLFVLVLVFAICWAPFHIDRLFFSFVEEWTES  
 LAAVFNLVHVVS GVLFYLLSSAVNP I IYNLLSRRFQAAFQNVISSFHKQWHSQHDPQLPPA  
 QRNIFLTECHFVELTEDIGPQFLCQSSVHNSHLPTALSSEQMSRTNYQSFHFNKT

**Table 6: IGS4A-64-protein of SEQ ID NO: 10 and SEQ ID NO: 12 (without three amino acids between brackets).**

30 (MSG) MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGV  
 IGNVLVCLVILQHQAMKTPTNYLFS LAVSDLLVLLLGM PLEVYEMWRNYPFLFGPVGCY  
 FKTALFETVCFASILSITTVSVERYVAILHPPFRAKLQSTRRRALRILGIVWGFSVLFSLP  
 NTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMA  
 LRLKKDKSLEADEGNANIQRPCRKSVNKMLSLWRS GVN PWLLCSTSSMWCQVSSST

## DESCRIPTION OF THE INVENTION

### Definitions

5       The following definitions are provided to facilitate understanding of certain terms used frequently herein.

      "IGS4" refers, among others, to a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 2 or SEQ ID NO: 4 (IGS4A) and SEQ ID NO: 6 or SEQ ID NO: 8 (IGS4B), or a variant thereof. Particularly preferred are polypeptides of IGS4B.

      "Receptor Activity" or "Biological Activity of the Receptor" refers to the metabolic or physiologic function of said IGS4 including similar activities or improved activities or these activities with decreased undesirable side effects. Also included are antigenic and immunogenic activities of said IGS4.

15       "IGS4-gene" refers to a polynucleotide comprising the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7 or variants thereof and/or their complements.

20       "Antibodies" as used herein includes polyclonal and monoclonal antibodies, chimeric, single chain, and humanized antibodies, as well as Fab fragments, including the products of a Fab or other immunoglobulin expression library.

25       "Isolated" means altered "by the hand of man" from the natural state and/or separated from the natural environment. Thus, if an "isolated" composition or substance that occurs in nature has been "isolated", it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living animal is not "isolated", but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein.

30       "Polynucleotide" generally refers to any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. "Polynucleotides" include, without limitation single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is a mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or  
35       a mixture of single- and double-stranded regions. In addition, "polynucleotide" may also include triple-stranded regions comprising RNA or DNA or both RNA and DNA. The term polynucleotide also includes DNAs or RNAs containing one or more modified bases and DNAs or RNAs with backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications has been made to DNA and RNA; thus, "polynucleotide"

embraces chemically, enzymatically or metabolically modified forms of polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells. "Polynucleotide" also embraces relatively short polynucleotides, often referred to as oligonucleotides.

5 "Polypeptide" refers to any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres. "Polypeptide" refers to short chains, commonly referred to as peptides, oligopeptides or oligomers, and to longer chains, generally referred to as proteins, and/or to combinations thereof. Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. "Polypeptides" include amino acid sequences modified either by  
10 natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well-described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying  
15 degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety,  
20 covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol; cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. See, for instance, PROTEINS - STRUCTURE AND MOLECULAR  
25 PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York, 1993 and Wold, F., Posttranslational Protein Modifications: Perspectives and Prospects, pgs. 1-12 in POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic  
30 Press, New York, 1983; Seifter et al., "Analysis for protein modifications and nonprotein cofactors", Meth. Enzymol. (1990) 182:626-646 and Rattan et al., "Protein Synthesis: Posttranslational Modifications and Aging", Ann. NY Acad. Sci. (1992) 663:48-62.

"Variant" as the term is used herein, is a polynucleotide or polypeptide that differs from a  
35 reference polynucleotide or polypeptide respectively, but retains essential properties such as essential biological, structural, regulatory or biochemical properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions

and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, additions, and deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis.

"Identity" is a measure of the identity of nucleotide sequences or amino acid sequences. In general, the sequences are aligned so that the highest order match is obtained. "Identity" per se has an art-recognized meaning and can be calculated using published techniques. See, e.g.: (COMPUTATIONAL MOLECULAR BIOLOGY, Lesk, A.M., ed., Oxford University Press, New York, 1988; BIOCOMPUTING: INFORMATICS AND GENOME PROJECTS, Smith, D.W., ed.; Academic Press, New York, 1993; COMPUTER ANALYSIS OF SEQUENCE DATA, PART I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; SEQUENCE ANALYSIS IN MOLECULAR BIOLOGY, von Heinje, G., Academic Press, 1987; and SEQUENCE ANALYSIS PRIMER, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). While there exist a number of methods to measure identity between two polynucleotide or polypeptide sequences, the term "identity" is well known to skilled artisans (Carillo, H., and Lipton, D., SIAM J. Applied Math. (1988) 48:1073). Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in Guide to Huge Computers, Martin J. Bishop, ed., Academic Press, San Diego, 1994, and Carillo, H., and Lipton, D., SIAM J. Applied Math. (1988) 48:1073. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux, J., et al., Nucleic Acids Research (1984) 12(1):387), BLASTP, BLASTN, FASTA (Atschul, S.F. et al., J. Molec. Biol. (1990) 215:403). The word "homology" may substitute for the word "identity".

As an illustration, by a polynucleotide having a nucleotide sequence having at least, for example, 95% "identity" to a reference nucleotide sequence of SEQ ID NO: 1 is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five nucleotide differences per each 100 nucleotides of the reference nucleotide sequence of SEQ ID NO: 1. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to any 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to any 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence, or in a number of nucleotides of up to any 5% of the total nucleotides in the

reference sequence there may be a combination of deletion, insertion and substitution. These mutations of the reference sequence may occur at the 5 or 3 terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

Similarly, by a polypeptide having an amino acid sequence having at least, for example, 95% "identity" to a reference amino acid sequence of SEQ ID NO: 2 is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid of SEQ ID NO: 2. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to any 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to any 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

## Polypeptides of the Invention

In one aspect, the present invention relates to IGS4 polypeptides (or IGS4 proteins). The IGS4 polypeptides include the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 and SEQ ID NO: 8 and the polypeptide having the amino acid sequence encoded by the DNA insert contained in the deposit no. CBS102221 or deposit no. CBS102222, deposited on September 24, 1999 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands; as well as polypeptides comprising the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8 and the polypeptide having the amino acid sequence encoded by the DNA insert contained in the deposit no. CBS102221 or deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands and polypeptides comprising the amino acid sequence which have at least 80% identity to that of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8 and/or the polypeptide having the amino acid sequence encoded by the DNA insert contained in the deposit no. CBS102221 or deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands over its entire length, and still more preferably at least 90% identity, and even still more preferably at least 95% identity to said amino acid sequences. Furthermore, those with at least 97%, in particular at least 99%, are highly preferred. Also included within IGS4 polypeptides are polypeptides having the amino acid sequence which has at least 80% identity to the polypeptide having the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8 or the polypeptide having the amino acid sequence encoded by the DNA insert contained in the deposit no. CBS102221 or deposit

no.CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands over its entire length, and still more preferably at least 90% identity, and even still more preferably at least 95% identity to SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8. Furthermore, those with at least 97%, in particular at least 99% are highly preferred. Preferably IGS4 polypeptides exhibit at least one biological activity of the receptor.

In an additional embodiment of the invention, the IGS4 polypeptides may be a part of a larger protein such as a fusion protein. It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification such as multiple histidine residues, sequences which aid in detection such as antigenic peptide tags (such as the haemagglutinin (HA) tag), or an additional sequence for stability during recombinant production.

Fragments of the IGS4 polypeptides are also included in the invention. A fragment is a polypeptide having an amino acid sequence that is the same as part of, but not all of, the amino acid sequence of the aforementioned IGS4 polypeptides. As with IGS4 polypeptides, fragments may be "free-standing," or comprised within a larger polypeptide of which they form a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20; 21-40, 41-60, 61-80, 81-100; and 101 to the end of IGS4 polypeptide. In this context "about" includes the particularly recited ranges larger or smaller by several, 5, 4, 3, 2 or 1 amino acid at either extreme or at both extremes.

Preferred fragments include, for example, truncation polypeptides having the amino acid sequence of IGS4 polypeptides, except for deletion of a continuous series of residues that includes the amino terminus, or a continuous series of residues that includes the carboxyl terminus or deletion of two continuous series of residues, one including the amino terminus and one including the carboxyl terminus. An example of a truncated polypeptide according to the present invention is the polypeptide of SEQ ID NO: 10 and SEQ ID NO: 12, which is encoded by the polynucleotide of SEQ ID NO: 9 respectively SEQ ID NO: 11. Also preferred are fragments characterized by structural or functional attributes such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Other preferred fragments are biologically active fragments. Biologically active fragments are those that mediate receptor activity, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Also included are those that are antigenic or immunogenic in an animal, especially in a human.

Thus, the polypeptides of the invention include polypeptides having an amino acid sequence at least 80% identical to that of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8 and/or the

polypeptide having the amino acid sequence encoded by the DNA insert contained in the deposit no. CBS102221 or the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands, or fragments thereof with at least 80% identity to the corresponding fragment. Preferably, all of these polypeptide fragments retain the biological activity of the receptor, including antigenic activity. Variants of the defined sequence and fragments also form part of the present invention. Preferred variants are those that vary from the referents by conservative amino acid substitutions -- i.e., those that substitute a residue with another of like characteristics. Typical such substitutions are among Ala, Val, Leu and Ile; among Ser and Thr; among the acidic residues Asp and Glu; among Asn and Gln; and among the basic residues Lys and Arg; or aromatic residues Phe and Tyr. Particularly preferred are variants in which several, 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination.

With regard to the polypeptides of the present invention it was also found that they show a high affinity binding for neuromedin U, in particular for neuromedin U-8 (an oligopeptide of 8 amino acids), neuromedin U-23 (an oligopeptide of 23 amino acids) and/or neuromedin U-25 (an oligopeptide of 25 amino acids). In the context of the present invention the term "high affinity" is understood as to describe a ligand binding showing log EC<sub>50</sub> values of at least below -6.00 (approx. 660 nM), preferably log EC<sub>50</sub> below -7.00 (approx. 55 nM), more preferably log EC<sub>50</sub> below -9.00 (approx. 500 pM to 1.2 nM), and most preferably log EC<sub>50</sub> below -10.00 (approx. 50-100 pM).

Two forms of the neuropeptide neuromedin U, neuromedin U-8 and neuromedin U-25, are described in the literature as uterus stimulating and hypertensive peptides (Minamino et al., 1985, Biochem. Biophys. Res. Commun. 130:1078-1085) being originally isolated from the porcine spinal cord. For neuromedin U-23, an oligopeptide of 23 amino acids, see for example: Okimura et al., Pept. Chem. (1995), Vol. Date 1994, 32:321-324; Salmon et al., J. Biol. Chem. (2000), 275(7), 4549-4554. Neuromedin U (NMU) was subsequently isolated from a number of species, e.g. from rat (NMU-23), human (NMU-25), frog (NMU-25), dog (NMU-8 and NMU-25), rabbit (NMU-25), and chicken (NMU-25). Thus, Domin et al. described the characterization of neuromedin U like immunoreactivity in rat, porcine, guinea pig and human tissue extracts using a specific radioimmunoassay (1986, Biochem. Biophys. Res. Commun. 140:1127-34). The primary structure of neuromedin U 23 from the rat ileum was established by Conlon et al. (1988, J. Neurochem. 51:988-991). Minamino et al. (1988, Biochem. Biophys. Res. Commun. 156:355-360) have isolated rat neuromedin U from the small intestine using mainly immunoaffinity chromatography and radioimmunoassay for pig neuromedin U-8, and the amino acid sequence of rat neuromedin U was determined by microsequence analysis and the structure was confirmed by synthesis. Although the C-terminal heptapeptide amide structure of pig neuromedin U is completely conserved in rat neuromedin U, the remainder of the peptide reveals nine amino acid replacements and two amino acid deletions when compared to pig neuromedin U-25. The distribution, primary structure, and relative biological activity of neuromedin U has been determined also in the frog *Rana temporaria* by Domin et al. (1989, J. Biol. Chem. 264:20881-20885) showing that the entire



sequence was found to be an icosapentapeptide which displays marked sequence similarity to both porcine and rat neuromedin U. In a further study Domin et al.(1992, Regul. Pept. 41:1-8) have purified an avian homolog of neuromedin U from the chicken. Microsequence analysis characterized the peptide to be 25 amino acid residues long, and chicken neuromedin U showed marked sequence similarity with the porcine peptide at its bioactive C-terminal region. Isolation, structural characterization and pharmacological activity of dog neuromedin U-25 was described by O'Harte et al. (1991 Peptides 12:11-15). Furthermore, for rabbit neuromedin U-25 it was found that it lacks conservation of a posttranslational processing site (Kage et al.,1991 Regul. Pept. 33:191-198); thus, in rabbit neuromedin U, the Arg16-Arg17 dibasic residue processing site that is found in pig and dog neuromedin U-25 is replaced by Arg-Gly, but this potential monobasic processing site is not utilized by cleavage enzyme(s) in the intestine.

Among the species studied the 5 amino acids at the C-terminus of the peptide were found to be almost totally conserved, suggesting that this region is of major importance. Thus, mammalian neuromedins share a common C-terminal sequence "-Phe-Leu-Phe-Arg-Pro-Arg-Asn-amide" which appears to be essential for its biological activities. NMU is distributed both in the gastrointestinal tract and the central nervous System (CNS). In the rat, the highest concentration of neuromedin (NMU) was found in the ileum, followed by the pituitary, hypothalamus, spinal cord, thyroid, and the genitourinary tract. Immunohistochemistry studies showed that NMU immunoreactivity in the gut was only found in nerve fibers, mainly in the myenteric and submucous plexuses, and in the mucosa of all areas except stomach while no NMU immunoreactivity was found in endocrine cells. In the rat brain, NMU immunoreactivity was found in fibers widespread throughout the brain with the exception of the cerebellum. Human and rat genes encoding NMU precursor have been isolated. Both encode NMU at the C-terminus and other potential peptide products in the middle (Lo et al., 1992, J. Mol. Endocrinol. 6:1538-1544; Austin et al., 1995, J. Mol. Endocrinol. 14:157-169). High affinity NMU binding was characterized in rat uterus, and was shown to be sensitive to GTP- $\gamma$ S (Nandha et al., 1993, Endocrinology 133:482-486), suggesting that a receptor for NMU should be a G-protein coupled receptor. Nevertheless, the physiological role of NMU remains largely unknown. Neuromedin U can cause potent contraction of smooth muscle, increase arterial blood pressure, modify intestinal ion transport, and at low doses stimulates the function and growth of the adrenal cortex. NMU was also shown to reduce the blood flow in superior enteric artery and portal vein while increase blood flow slightly in pancreatic tissue.

Furthermore, according to the international patent application WO 90/01330 the neuromedins U-8 and U-25 are described to be suitable in the treatment of disorders of the gastrointestinal tract, e.g. being useful in the selective reduction of blood flow to the gastrointestinal tract, in the treatment of gastrointestinal bleeding and postprandial hypotension.

The IGS4 polypeptides of the present invention have been identified as a G-protein coupled receptor responsive to neuromedin U or ligands sufficiently similar thereto. Thus the IGS4 receptor, in



particular the IGS4B receptor, responsive to neuromedin U will greatly facilitate the understanding of the physiological mechanisms of neuromedin U and other ligands sufficiently similar thereto, as well as of related diseases.

5 The tissue distribution of the polypeptides of the present invention and the expression levels are shown in the Figures 5-8, from which the skilled artisan can estimate the localisation and relevance of expression. For instance, with regard to the tissue distribution of the polypeptides of the present invention it was found, e.g. by MTE (multiple tissue expression) analysis, Northern blot analysis and  
10 Quantitative RT-PCR expression analysis that the IGS4 polypeptides of the present invention particularly are brought to expression with a medium level (relative to expression in testis as 100% in MTE blot, or in spinal cord as 100% in Quantitative RT-PCR analysis, respectively) e.g. in brain, skeletal muscle, cerebellum, thymus, medulla, thyroid, trachea, thalamus, substantia nigra, corpus callosum, caudate nucleus, pons, nucleus accumbens, fetal brain and stomach; and with a relevant level (if being detectable by Quantitative RT-PCR analysis) e.g. in heart, lung, and prostate. For instance, expression  
15 levels are considered to be medium if they amount at least 20% of the expression value found for the by far highest expression (set as 100%) in testis or spinal cord. For instance, expression levels are considered to be relevant if expression could be detected at least via Quantitative RT-PCR analysis. It will be appreciated that expression levels indicated for any organ are average values of expression levels in the specific tissues and cell types constituting the organ. Thus, if an expression level is just  
20 found to be relevant with respect to an organ, this does not necessarily exclude medium or even high expression levels locally within a specific region, e.g. in a specific tissue and/or cell type, of the organ.

These results suggest that IGS4 polypeptides preferably play a role in the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), in the  
25 gastrointestinal system and/or in the cardiovascular system and/or in skeletal muscle and/or in the thyroid, and/or also in lung diseases, immunological diseases and disorders of the genitourinary system.

Thus, in a further embodiment the invention pertains also to an isolated IGS4 polypeptide comprising an amino acid sequence of a neuromedin receptor protein, preferably of a mammalian  
30 neuromedin receptor protein, said protein exhibiting high affinity binding for neuromedin U, preferably for neuromedin U-8, for neuromedin U-23 and/or for neuromedin U-25. Particularly, the isolated IGS4 polypeptide comprising an amino acid sequence of a neuromedin receptor protein, is a protein exhibiting expression (being at least detectable via Northern and/or MTE and/or Quantitative RT-PCR analysis) in brain, skeletal muscle, cerebellum, testis, corpus callosum, spinal cord, substantia nigra, medulla,  
35 thalamus, caudate nucleus, pons, nucleus accumbens, fetal brain, stomach, heart, thyroid gland, lung, thymus, prostate and/or in trachea. In a variant of this embodiment the invention pertains to an isolated IGS4 polypeptide comprising an amino acid sequence of a neuromedin receptor protein, preferably of a mammalian neuromedin receptor protein, said protein exhibiting high affinity binding for neuromedin U, preferably for neuromedin U-8, for neuromedin U-23 and/or for neuromedin U-25, said protein exhibiting

expression (being at least detectable via Northern and/or MTE and/or Quantitative RT-PCR analysis) in brain, skeletal muscle, cerebellum, testis, corpus callosum, spinal cord, substantia nigra, medulla, thalamus, caudate nucleus, pons, nucleus accumbens, fetal brain, stomach, heart, thyroid gland, lung, thymus, prostate and/or in trachea, and said amino acid sequence being selected from the group of amino acid sequence as already defined supra.

The IGS4 polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Methods for preparing such polypeptides are well known in the art.

### Polynucleotides of the Invention

A further aspect of the invention relates to IGS4 polynucleotides. IGS4 polynucleotides include isolated polynucleotides which encode the IGS4 polypeptides (including IGS4A and IGS4B) and fragments, and polynucleotides closely related thereto. More specifically, the IGS4 polynucleotide of the invention includes a polynucleotide comprising the nucleotide sequence contained in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7 encoding a IGS4A polypeptide of SEQ ID NO: 2 or of SEQ ID NO: 4 and a IGS4B polypeptide of SEQ ID NO: 6 or of SEQ ID NO: 8 respectively, polynucleotides having the particular sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7 and polynucleotides which essentially correspond to the DNA insert contained in the deposit no. CBS102221 or the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands.

IGS4 polynucleotides further include polynucleotides comprising a nucleotide sequence that has at least 80% identity over its entire length to a nucleotide sequence encoding the IGS4 polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8, a polynucleotide comprising a nucleotide sequence that is at least 80% identical to that of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7 over its entire length and a polynucleotide which essentially correspond to the DNA insert contained in the deposit no. CBS102221 or the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands.

In this regard, polynucleotides with at least 90% identity are particularly preferred, and those with at least 95% are especially preferred. Furthermore, those with at least 97% are highly preferred and those with at least 98-99% are most highly preferred, with at least 99% being the most preferred. Also included under IGS4 polynucleotides are a nucleotide sequence which has sufficient identity to a nucleotide sequence contained in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7 or to the DNA insert contained in the deposit no. CBS102221 or in the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands to hybridize under conditions useable

for amplification or for use as a probe or marker. The invention also provides polynucleotides which are complementary to such IGS4 polynucleotides.

IGS4 of the invention is structurally related to other proteins of the G-protein coupled receptor family, as shown by the results of BLAST searches in the public databases. The amino acid sequence of Table 1 (SEQ ID NO: 2) has about 46 % identity (using BLAST, Altschul S.F. et al. [1997], Nucleic Acids Res. 25:3389-3402) over most of its length (316 amino acid residues) with a human orphan G-protein coupled receptor (Accession # O43664, Tan et al., Genomics 52(2):223-229 (1998)). There is 27 % homology (over amino acid residues 61-349 ) to the rat neurotensin 1 receptor (Accession # P20789 Tanaka K. et al, Neuron 4:847-854 (1990)). The nucleotide sequence of Table 1 (SEQ ID NO: 1) is 63 % identical to an orphan G-protein coupled receptor over nucleotide residues 120-864 (Accession # AF044600, corresponding with the protein sequence O43664). Furthermore, there is 53 % identity to the human growth hormone secretagogue receptor over residues 94-1137 (Howard A.D. et al, Science 273:974-977(1996)). Thus, IGS4 polypeptides and polynucleotides of the present invention are expected to have, inter alia, similar biological functions/properties to their homologous polypeptides and polynucleotides, and their utility is obvious to anyone skilled in the art.

Polynucleotides of the invention can be obtained from natural sources such as genomic DNA. In particular, degenerated PCR primers can be designed that encode conserved regions within a particular GPCR gene subfamily. PCR amplification reactions on genomic DNA or cDNA using the degenerate primers will result in the amplification of several members (both known and novel) of the gene family under consideration (the degenerated primers must be located within the same exon, when a genomic template is used). (Libert et al., Science, 1989, 244: 569-572). Polynucleotides of the invention can also be synthesized using well-known and commercially available techniques (e.g. F.M. Ausubel et al, 2000, Current Protocols in Molecular Biology).

The nucleotide sequence encoding the IGS4 polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8 may be identical to the polypeptide encoding sequence contained in SEQ ID NO: 1 (nucleotide number 55 to 1299) or SEQ ID NO: 3 (nucleotide number 64 to 1299), or SEQ ID NO: 5 (nucleotide number 55 to 1299) or SEQ ID NO: 7 (nucleotide number 64 to 1299) respectively, or it may be a different nucleotide sequence, which as a result of the redundancy (degeneracy) of the genetic code might also show alterations compared to the polypeptide encoding sequence contained in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7, but also encodes the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8, respectively.

In a further embodiment the invention pertains to an isolated nucleotide sequence encoding an IGS4 neuromedin receptor protein, preferably encoding a mammalian neuromedin receptor protein, said protein exhibiting high affinity binding for neuromedin U, preferably for neuromedin U-8, for neuromedin U-23 and/or for neuromedin U-25. Particularly, the isolated nucleotide sequence encodes an IGS4

neuromedin receptor protein which is a protein exhibiting expression (being at least detectable via Northern and/or MTE and/or Quantitative RT-PCR analysis) in brain, skeletal muscle, cerebellum, testis, corpus callosum, spinal cord, substantia nigra, medulla, thalamus, caudate nucleus, pons, nucleus accumbens, fetal brain, stomach, heart, thyroid gland, lung, thymus, prostate and/or in trachea. In a  
5 variant of this embodiment the invention pertains to an isolated nucleotide sequence encoding an IGS4 neuromedin receptor protein, preferably encoding a mammalian neuromedin receptor protein, said protein exhibiting high affinity binding for neuromedin U, preferably for neuromedin U-8, for neuromedin U-23 and/or for neuromedin U-25, said protein exhibiting expression (being at least detectable via Northern and/or MTE and/or Quantitative RT-PCR analysis) in brain, skeletal muscle, cerebellum, testis,  
10 corpus callosum, spinal cord, substantia nigra, medulla, thalamus, caudate nucleus, pons, nucleus accumbens, fetal brain, stomach, heart, thyroid gland, lung, thymus, prostate and/or in trachea, and said nucleotide sequence being selected from the group of nucleotide sequences as already defined supra.

When the polynucleotides of the invention are used for the recombinant production of the IGS4  
15 polypeptide, the polynucleotide may include the coding sequence for the mature polypeptide or a fragment thereof, by itself; the coding sequence for the mature polypeptide or fragment in reading frame with other coding sequences, such as those encoding a leader or secretory sequence, a pre-, or pro- or prepro- protein sequence, or other fusion peptide portions. For example, a marker sequence which facilitates purification of the fused polypeptide can be encoded. In certain preferred embodiments of this  
20 aspect of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz et al., Proc. Natl. Acad. Sci USA (1989) 86:821-824, or is an HA tag. The polynucleotide may also contain non-coding 5' and 3' sequences, such as transcribed, non-translated sequences, splicing and polyadenylation signals, ribosome binding sites and sequences that stabilize mRNA.

25 Further preferred embodiments are polynucleotides encoding IGS4 variants comprising the amino acid sequence of the IGS4 polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8 in which several, 5-10, 1-5, 1-3, 1-2 or 1 amino acid residues are substituted, deleted or added, in any combination.

30 The polynucleotides of the invention can be engineered using methods generally known in the art in order to alter IGS4-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to  
35 engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create amino acid substitutions, create new restriction sites, alter modification (e.g. glycosylation or phosphorylation) patterns, change codon preference, produce splice variants, and so forth.

The present invention further relates to polynucleotides that hybridize to the herein above-described sequences. In this regard, the present invention especially relates to polynucleotides which hybridize under stringent conditions to the polynucleotides described above. As herein used, the term "stringent conditions" means hybridization will occur only if there is at least 80%, and preferably at least 90%, and more preferably at least 95%, yet even more preferably at least 97%, in particular at least 99% identity between the sequences.

Polynucleotides of the invention, which are identical or sufficiently identical to a nucleotide sequence contained in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7 or a fragment thereof, may be used as hybridization probes for cDNA and genomic DNA, to isolate full-length cDNAs and genomic clones encoding IGS4 and to isolate cDNA and genomic clones of other genes (including genes encoding homologs and orthologs from species other than human) that have a high sequence similarity to the IGS4 gene. People skilled in the art are well aware of such hybridization techniques. Typically these nucleotide sequences are 80% identical, preferably 90% identical, more preferably 95% identical to that of the referent. The probes generally will comprise at least 5 nucleotides, and preferably at least 8 nucleotides, and more preferably at least 10 nucleotides, yet even more preferably at least 12 nucleotides, in particular at least 15 nucleotides. Most preferred, such probes will have at least 30 nucleotides and may have at least 50 nucleotides. Particularly preferred probes will range between 30 and 50 nucleotides.

One embodiment, to obtain a polynucleotide encoding the IGS4 polypeptide, including homologs and orthologs from species other than human, comprises the steps of screening an appropriate library under stringent hybridization conditions with a labeled probe having the SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7 or a fragment thereof, and isolating full-length cDNA and genomic clones containing said polynucleotide sequence. Such hybridization techniques are well known to those of skill in the art. Stringent hybridization conditions are as defined above or alternatively conditions under overnight incubation at 42 °C in a solution comprising: 50% formamide, 5xSSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10 % dextran sulfate (w/v), and 20 microgram/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1xSSC at about 65°C.

The polynucleotides and polypeptides of the present invention may be used as research reagents and materials for discovery of treatments and diagnostics to animal and human disease.

### **Vectors, Host Cells, Expression**

The present invention also relates to vectors which comprise a polynucleotide or polynucleotides of the present invention, and host cells which are genetically engineered with vectors of the invention and to the production of polypeptides of the invention by recombinant techniques. Cell-free translation

systems can also be used to produce such proteins using RNAs derived from the DNA constructs of the present invention.

5 For recombinant production, host cells can be genetically engineered to incorporate expression systems or portions thereof for polynucleotides of the present invention. Introduction of polynucleotides into host cells can be effected by methods described in many standard laboratory manuals, such as Davis et al., BASIC METHODS IN MOLECULAR BIOLOGY (1986) and Sambrook et al., MOLECULAR CLONING: A LABORATORY MANUAL, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989) such as calcium phosphate transfection, DEAE-dextran mediated transfection, 10 transfection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction or infection.

Representative examples of appropriate hosts include bacterial cells, such as streptococci, staphylococci, E. coli, Streptomyces and Bacillus subtilis cells; fungal cells, such as yeast cells and 15 Aspergillus cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, HEK 293 and Bowes melanoma cells; and plant cells.

A great variety of expression systems can be used. Such systems include, among others, chromosomal, episomal and virus-derived systems, e.g., vectors derived from bacterial plasmids, from 20 bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids. The expression systems may contain control regions that regulate as 25 well as engender expression. Generally, any system or vector suitable to maintain, propagate or express polynucleotides to produce a polypeptide in a host may be used. The appropriate nucleotide sequence may be inserted into an expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in Sambrook et al., MOLECULAR CLONING, A LABORATORY MANUAL (supra).

30 For secretion of the translated protein into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment, appropriate secretion signals may be incorporated into the desired polypeptide. These signals may be endogenous to the polypeptide or they may be heterologous signals, i.e. derived from a different species.

35 If the IGS4 polypeptide is to be expressed for use in screening assays, generally, it is preferred that the polypeptide be produced at the surface of the cell. In this event, the cells may be harvested prior to use in the screening assay. In case the affinity or functional activity of the IGS4 polypeptide is modified by receptor activity modifying proteins (RAMP), coexpression of the relevant RAMP most likely

at the surface of the cell is preferred and often required. Also in this event harvesting of cells expressing the IGS4 polypeptide and the relevant RAMP prior to use in screening assays is required. If the IGS4 polypeptide is secreted into the medium, the medium can be recovered in order to recover and purify the polypeptide; if produced intracellularly, the cells must first be lysed before the polypeptide is recovered.

5 Membranes expressing the IGS4 polypeptide can be recovered by methods that are well known to a person skilled in the art. In general, such methods include harvesting of the cells expressing the IGS4 polypeptide and homogenization of the cells by a method such as, but not limited to, pottering. The membranes may be recovered by washing the suspension one or several times.

10 IGS4 polypeptides can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well-known techniques for refolding  
15 proteins may be employed to regenerate active conformation when the polypeptide is denatured during isolation and or purification.

### Diagnostic Assays

20 This invention also relates to the use of IGS4 polynucleotides for use as diagnostic reagents. Detection of a mutated form of the IGS4 gene associated with a dysfunction will provide a diagnostic tool that can add to or define a diagnosis of a disease or susceptibility to a disease which results from under-expression, over-expression or altered expression of IGS4. Also in this event co-expression of relevant receptor activity modifying proteins can be required to obtain diagnostic assays of desired quality.  
25 Individuals carrying mutations in the IGS4 gene may be detected at the DNA level by a variety of techniques.

Nucleic acids for diagnosis may be obtained from a subject's cells, such as from blood, urine, saliva, tissue biopsy or autopsy material. The genomic DNA may be used directly for detection or may  
30 be amplified enzymatically by using PCR or other amplification techniques prior to analysis. RNA or cDNA may also be used in similar fashion. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype. Point mutations can be identified by hybridizing amplified DNA to labeled IGS4 nucleotide sequences. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures.  
35 DNA sequence differences may also be detected by alterations in electrophoretic mobility of DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing. See, e.g., Myers et al., Science (1985) 230:1242. Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and S1 protection or the chemical cleavage method. See Cotton et al., Proc. Natl. Acad. Sci. USA (1985) 85: 4397-4401. In another embodiment, an array of



oligonucleotide probes comprising the IGS4 nucleotide sequence or fragments thereof can be constructed to conduct efficient screening of e.g., genetic mutations. Array technology methods are well known and have general applicability and can be used to address a variety of questions in molecular genetics including gene expression, genetic linkage, and genetic variability. (See for example: M.Chee et al., Science, Vol 274, pp 610-613 (1996)).

The diagnostic assays offer a process for diagnosing or determining a susceptibility to PNS, psychiatric and CNS disorders, including schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive disorder (OCD), post traumatic stress disorder (PTSD), phobia and panic, major depressive disorder, bipolar disorder, Parkinson's disease, general anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer disease/dementia and other neurodegenerative diseases, severe mental retardation, dyskinesias, Huntington's disease, Tourett's syndrome, tics, tremor, dystonia, spasms, anorexia, bulimia, stroke, addiction/dependency/craving, sleep disorder, epilepsy, migraine; attention deficit/hyperactivity disorder (ADHD); cardiovascular diseases, including heart failure, angina pectoris, arrhythmias, myocardial infarction, cardiac hypertrophy, hypotension, hypertension – e.g. essential hypertension, renal hypertension, or pulmonary hypertension, thrombosis, arteriosclerosis, cerebral vasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney disease – e.g. renal failure; dyslipidemias; obesity; emesis; gastrointestinal disorders, including irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), gastroesophageal reflux disease (GERD), motility disorders and conditions of delayed gastric emptying, such as post operative or diabetic gastroparesis, and diabetes, ulcers – e.g. gastric ulcer; diarrhoea; other diseases including osteoporosis; inflammations; infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; pain; cancers; chemotherapy induced injury; tumor invasion; immune disorders; urinary retention; asthma; allergies; arthritis; benign prostatic hypertrophy; endotoxin shock; sepsis; complication of diabetes mellitus; and gynaecological disorders, through detection of mutation in the IGS4 gene by the methods described. According to the present invention, the diagnostic assays offer in particular a process for diagnosing or determining a susceptibility to disorders of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), disorders of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal muscle and/or of the thyroid, and/or also to lung diseases, immunological diseases and disorders of the genitourinary system.

In addition, PNS, psychiatric and CNS disorders, including schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive disorder (OCD), post traumatic stress disorder (PTSD), phobia and panic, major depressive disorder, bipolar disorder, Parkinson's disease, general anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer disease/dementia and other neurodegenerative diseases, severe mental retardation, dyskinesias, Huntington's disease, Tourett's syndrome, tics, tremor, dystonia, spasms, anorexia, bulimia, stroke, addiction/dependency/craving, sleep disorder, epilepsy, migraine; attention deficit/hyperactivity disorder (ADHD); cardiovascular



diseases, including heart failure, angina pectoris, arrhythmias, myocardial infarction, cardiac hypertrophy, hypotension, hypertension – e.g. essential hypertension, renal hypertension, or pulmonary hypertension, thrombosis, arteriosclerosis, cerebral vasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney disease – e.g. renal failure; dyslipidemias; obesity; emesis; gastrointestinal disorders, including irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), gastroesophageal reflux disease (GERD), motility disorders and conditions of delayed gastric emptying, such as post operative or diabetic gastroparesis, and diabetes, ulcers – e.g. gastric ulcer; diarrhoea; other diseases including osteoporosis; inflammations; infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; pain; cancers; chemotherapy induced injury; tumor invasion; immune disorders; urinary retention; asthma; allergies; arthritis; benign prostatic hypertrophy; endotoxin shock; sepsis; complication of diabetes mellitus; and gynaecological disorders, can be diagnosed by methods comprising determining from a sample derived from a subject an abnormally decreased or increased level of the IGS4 polypeptide or IGS4 mRNA. In particular disorders of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), disorders of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal muscle and/or of the thyroid, and/or also lung diseases, immunological diseases and disorders of the genitourinary system can be diagnosed by methods comprising determining from a sample derived from a subject an abnormally decreased or increased level of the IGS4 polypeptide or IGS4 mRNA. Decreased or increased expression can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, such as, for example, PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods. Assay techniques that can be used to determine levels of a protein, such as an IGS4, in a sample derived from a host are well known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

In another aspect, the present invention relates to a diagnostic kit for a disease or susceptibility to a disease, particularly PNS, psychiatric and CNS disorders, including schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive disorder (OCD), post traumatic stress disorder (PTSD), phobia and panic, major depressive disorder, bipolar disorder, Parkinson's disease, general anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer disease/dementia and other neurodegenerative diseases, severe mental retardation, dyskinesias, Huntington's disease, Tourett's syndrome, tics, tremor, dystonia, spasms, anorexia, bulimia, stroke, addiction/dependency/craving, sleep disorder, epilepsy, migraine; attention deficit/hyperactivity disorder (ADHD); cardiovascular diseases, including heart failure, angina pectoris, arrhythmias, myocardial infarction, cardiac hypertrophy, hypotension, hypertension – e.g. essential hypertension, renal hypertension, or pulmonary hypertension, thrombosis, arteriosclerosis, cerebral vasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney disease – e.g. renal failure; dyslipidemias; obesity; emesis; gastrointestinal

disorders, including irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), gastroesophageal reflux disease (GERD), motility disorders and conditions of delayed gastric emptying, such as post operative or diabetic gastroparesis, and diabetes, ulcers – e.g. gastric ulcer; diarrhoea; other diseases including osteoporosis; inflammations; infections such as bacterial, fungal, protozoan and viral

5 infections, particularly infections caused by HIV-1 or HIV-2; pain; cancers; chemotherapy induced injury; tumor invasion; immune disorders; urinary retention; asthma; allergies; arthritis; benign prostatic hypertrophy; endotoxin shock; sepsis; complication of diabetes mellitus; and gynaecological disorders, which comprises:

- 10 (a) an IGS4 polynucleotide, preferably the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7, or a fragment thereof; and/or
- (b) a nucleotide sequence complementary to that of (a); and/or
- (c) an IGS4 polypeptide, preferably the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or of SEQ ID NO: 8, or a fragment thereof; and/or
- 15 (d) an antibody to an IGS4 polypeptide, preferably to the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or of SEQ ID NO: 8; and/or
- (e) a RAMP polypeptide required for the relevant biological or antigenic properties of an IGS4 polypeptide

It will be appreciated that in any such kit, (a), (b), (c) (d) or (e) may comprise a substantial component.

20 Preferably the present invention relates to a diagnostic kit for diagnosing or determining a disease or a susceptibility to a disease of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), a disease of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal muscle and/or of the thyroid, and/or also lung diseases, immunological diseases and disorders of the genitourinary system.

### 25 Chromosome Assays

The nucleotide sequences of the present invention are also valuable for chromosome identification. The sequence is specifically targeted to and can hybridize with a particular location on an

30 individual human chromosome. The mapping of relevant sequences to chromosomes according to the present invention is an important first step in correlating those sequences with gene associated disease. Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins

35 University Welch Medical Library). The relationship between genes and diseases that have been mapped to the same chromosomal region are then identified through linkage analysis (coinheritance of physically adjacent genes).

The differences in the cDNA or genomic sequence between affected and unaffected individuals can also be determined. If a mutation is observed in some or all of the affected individuals but not in any normal individuals, then the mutation is likely to be the causative agent of the disease.

## Antibodies

The polypeptides of the invention or their fragments or analogs thereof, or cells expressing them if required together with relevant RAMP's, may also be used as immunogens to produce antibodies immunospecific for the IGS4 polypeptides. The term "immunospecific" means that the antibodies have substantiall greater affinity for the polypeptides of the invention than their affinity for other related polypeptides in the prior art.

Antibodies generated against the IGS4 polypeptides may be obtained by administering the polypeptides or epitope-bearing fragments, analogs or cells to an animal, preferably a nonhuman, using routine protocols. For preparation of monoclonal antibodies, any technique, which provides antibodies produced by continuous cell line cultures, may be used. Examples include the hybridoma technique (Kohler, G. and Milstein, C., Naure (1975) 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today (1983) 4:72) and the EBV-hybridoma technique (Cole et al., MONOCLONAL ANTIBODIES AND CANCER THERAPY, pp. 77-96, Alan R. Liss, Inc., 1985).

The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptide or to purify the polypeptides by affinity chromatography.

Antibodies against IGS4 polypeptides as such, or against IGS4 polypeptide-RAMP complexes, may also be employed to treat PNS, psychiatric and CNS disorders, including schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive disorder (OCD), post traumatic stress disorder (PTSD), phobia and panic, major depressive disorder, bipolar disorder, Parkinson's disease, general anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer disease/dementia and other neurodegenerative diseases, severe mental retardation, dyskinesias, Huntington's disease, Tourett's syndrome, tics, tremor, dystonia, spasms, anorexia, bulimia, stroke, addiction/dependency/craving, sleep disorder, epilepsy, migraine; attention deficit/hyperactivity disorder (ADHD); cardiovascular diseases, including heart failure, angina pectoris, arrhythmias, myocardial infarction, cardiac hypertrophy, hypotension, hypertension – e.g. essential hypertension, renal hypertension, or pulmonary hypertension, thrombosis, arteriosclerosis, cerebral vasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney disease – e.g. renal failure; dyslipidemias; obesity; emesis; gastrointestinal disorders, including irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), gastroesophageal reflux disease (GERD), motility disorders and conditions of delayed gastric emptying, such as post operative or diabetic gastroparesis, and diabetes, ulcers – e.g. gastric ulcer; diarrhoea; other diseases including osteoporosis; inflammations; infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; pain; cancers; chemotherapy induced injury; tumor invasion; immune disorders; urinary retention; asthma; allergies; arthritis; benign prostatic hypertrophy; endotoxin shock;

sepsis; complication of diabetes mellitus; and gynaecological disorders, among others. Preferably the antibodies of the present invention may be used to treat disorders of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), disorders of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal muscle and/or of the thyroid, and/or also to treat lung diseases, immunological diseases and disorders of the genitourinary system.

### Animals

Another aspect of the invention relates to non-human animal-based systems which act as models for disorders arising from aberrant expression or activity of IGS4. Non-human animal-based model systems may also be used to further characterize the activity of the IGS4 gene. Such systems may be utilized as part of screening strategies designed to identify compounds which are capable to treat IGS4 based disorders such as PNS, psychiatric and CNS disorders, including schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive disorder (OCD), post traumatic stress disorder (PTSD), phobia and panic, major depressive disorder, bipolar disorder, Parkinson's disease, general anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer disease/dementia and other neurodegenerative diseases, severe mental retardation, dyskinesias, Huntington's disease, Tourett's syndrome, tics, tremor, dystonia, spasms, anorexia, bulimia, stroke, addiction/dependency/craving, sleep disorder, epilepsy, migraine; attention deficit/hyperactivity disorder (ADHD); cardiovascular diseases, including heart failure, angina pectoris, arrhythmias, myocardial infarction, cardiac hypertrophy, hypotension, hypertension – e.g. essential hypertension, renal hypertension, or pulmonary hypertension, thrombosis, arteriosclerosis, cerebral vasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney disease – e.g. renal failure; dyslipidemias; obesity; emesis; gastrointestinal disorders, including irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), gastroesophageal reflux disease (GERD), motility disorders and conditions of delayed gastric emptying, such as post operative or diabetic gastroparesis, and diabetes, ulcers – e.g. gastric ulcer; diarrhoea; other diseases including osteoporosis; inflammations; infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; pain; cancers; chemotherapy induced injury; tumor invasion; immune disorders; urinary retention; asthma; allergies; arthritis; benign prostatic hypertrophy; endotoxin shock; sepsis; complication of diabetes mellitus; and gynaecological disorders. In particular, the systems may be utilized as part of screening strategies designed to identify compounds which are capable in particular to treat IGS4 based disorders of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), disorders of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal muscle and/or of the thyroid, and/or also to treat lung diseases, immunological diseases and disorders of the genitourinary system. In this way the animal-based models may be used to identify pharmaceutical compounds, therapies and interventions which may be effective in treating disorders of aberrant expression or

activity of IGS4. In addition such animal models may be used to determine the LD<sub>50</sub> and the ED<sub>50</sub> in animal subjects. These data may be used to determine the *in vivo* efficacy of potential IGS4 disorder treatments.

Animal-based model systems of IGS4 based disorders, based on aberrant IGS4 expression or activity, may include both non-recombinant animals as well as recombinantly engineered transgenic animals.

Animal models for IGS4 disorders may include, for example, genetic models. Animal models exhibiting IGS4 based disorder-like symptoms may be engineered by utilizing, for example, IGS4 sequences such as those described, above, in conjunction with techniques for producing transgenic animals that are well known to persons skilled in the art. For example, IGS4 sequences may be introduced into, and overexpressed and/or misexpressed in, the genome of the animal of interest, or, if endogenous IGS4 sequences are present, they may either be overexpressed, misexpressed, or, alternatively, may be disrupted in order to underexpress or inactivate IGS4 gene expression.

In order to overexpress or misexpress a IGS4 gene sequence, the coding portion of the IGS4 gene sequence may be ligated to a regulatory sequence which is capable of driving high level gene expression or expression in a cell type in which the gene is not normally expressed in the animal type of interest. Such regulatory regions will be well known to those skilled in the art, and may be utilized in the absence of undue experimentation.

For underexpression of an endogenous IGS4 gene sequence, such a sequence may be isolated and engineered such that when reintroduced into the genome of the animal of interest, the endogenous IGS4 gene alleles will be inactivated, or "knocked-out". Preferably, the engineered IGS4 gene sequence is introduced via gene targeting such that the endogenous IGS4 sequence is disrupted upon integration of the engineered IGS4 gene sequence into the animal's genome. Gene targeting is discussed, below, in this section.

Animals of any species, including, but not limited to, mice, rats, rabbits, squirrels, guinea-pigs, pigs, micro-pigs, goats, and non-human primates, e.g., baboons, monkeys, and chimpanzees may be used to generate animal models of IGS4 related disorders.

Any technique known in the art may be used to introduce a IGS4 transgene into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to pronuclear microinjection (Hoppe, P.C. and Wagner, T.E., 1989, U.S. Pat. No. 4,873,191); retrovirus mediated gene transfer into germ lines (van der Putten et al., Proc. Natl. Acad. Sci., USA 82:6148-6152, 1985); gene targeting in embryonic stem cells (Thompson et al., Cell 56:313-321, 1989,); electroporation of embryos (Lo, Mol. Cell. Biol. 3:1803-1814, 1983); and sperm-mediated gene transfer (Lavitrano et al.,

Cell 57:717-723, 1989); etc. For a review of such techniques, see Gordon, Transgenic Animals, Intl. Rev. Cytol.115:171-229, 1989, which is incorporated by reference herein in its entirety.

5 The present invention provides for transgenic animals that carry the IGS4 transgene in all their cells, as well as animals which carry the transgene in some, but not all their cells, i.e., mosaic animals. (See, for example, techniques described by Jakobovits, Curr. Biol. 4:761-763, 1994) The transgene may be integrated as a single transgene or in concatamers, e.g., head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching of Lasko et al. (Lasko, M. et al., Proc. Natl. Acad. Sci. USA 89:6232-  
10 6236, 1992).

The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art.

15 When it is desired that the IGS4 transgene be integrated into the chromosomal site of the endogenous IGS4 gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous IGS4 gene of interest (e.g., nucleotide sequences of the mouse IGS4 gene) are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of, the  
20 nucleotide sequence of the endogenous IGS4 gene or gene allele. The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous gene of interest in only that cell type, by following, for example, the teaching of Gu et al. (Gu, H. et al., Science 265:103-106, 1994). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art.

25 Once transgenic animals have been generated, the expression of the recombinant IGS4 gene and protein may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to analyze animal tissues to assay whether integration of the transgene has taken place. The level of mRNA expression of the IGS4 transgene in the tissues of the  
30 transgenic animals may also be assessed using techniques which include but are not limited to Northern blot analysis of tissue samples obtained from the animal, in situ hybridization analysis, and RT-PCR. Samples of target gene-expressing tissue, may also be evaluated immunocytochemically using antibodies specific for the target gene transgene product of interest. The IGS4 transgenic animals that express IGS4 gene mRNA or IGS4 transgene peptide (detected immunocytochemically, using  
35 antibodies directed against target gene product epitopes) at easily detectable levels may then be further evaluated to identify those animals which display characteristic IGS4 based disorder symptoms.

Once IGS4 transgenic founder animals are produced (i.e., those animals which express IGS4 proteins in cells or tissues of interest, and which, preferably, exhibit symptoms of IGS4 based disorders),



they may be bred, inbred, outbred, or crossbred to produce colonies of the particular animal. Examples of such breeding strategies include but are not limited to: outbreeding of founder animals with more than one integration site in order to establish separate lines; inbreeding of separate lines in order to produce compound IGS4 transgenics that express the IGS4 transgene of interest at higher levels because of the effects of additive expression of each IGS4 transgene; crossing of heterozygous transgenic animals to produce animals homozygous for a given integration site in order to both augment expression and eliminate the possible need for screening of animals by DNA analysis; crossing of separate homozygous lines to produce compound heterozygous or homozygous lines; breeding animals to different inbred genetic backgrounds so as to examine effects of modifying alleles on expression of the IGS4 transgene and the development of IGS4-like symptoms. One such approach is to cross the IGS4 transgenic founder animals with a wild type strain to produce an F1 generation that exhibits IGS4 related disorder-like symptoms, such as those described above. The F1 generation may then be inbred in order to develop a homozygous line, if it is found that homozygous target gene transgenic animals are viable.

## **Vaccines**

Another aspect of the invention relates to a method for inducing an immunological response in a mammal which comprises administering to (for example by inoculation) the mammal the IGS4 polypeptide, or a fragment thereof, if required together with a RAMP polypeptide, adequate to produce antibody and/or T cell immune response to protect said animal from PNS, psychiatric and CNS disorders, including schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive disorder (OCD), post traumatic stress disorder (PTSD), phobia and panic, major depressive disorder, bipolar disorder, Parkinson's disease, general anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer disease/dementia and other neurodegenerative diseases, severe mental retardation, dyskinesias, Huntington's disease, Tourett's syndrome, tics, tremor, dystonia, spasms, anorexia, bulimia, stroke, addiction/dependency/craving, sleep disorder, epilepsy, migraine; attention deficit/hyperactivity disorder (ADHD); cardiovascular diseases, including heart failure, angina pectoris, arrhythmias, myocardial infarction, cardiac hypertrophy, hypotension, hypertension – e.g. essential hypertension, renal hypertension, or pulmonary hypertension, thrombosis, arteriosclerosis, cerebral vasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney disease – e.g. renal failure; dyslipidemias; obesity; emesis; gastrointestinal disorders, including irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), gastroesophageal reflux disease (GERD), motility disorders and conditions of delayed gastric emptying, such as post operative or diabetic gastroparesis, and diabetes, ulcers – e.g. gastric ulcer; diarrhoea; other diseases including osteoporosis; inflammations; infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; pain; cancers; chemotherapy induced injury; tumor invasion; immune disorders; urinary retention; asthma; allergies; arthritis; benign prostatic hypertrophy; endotoxin shock; sepsis; complication of diabetes mellitus; and gynaecological disorders, among others. Yet another aspect of the invention relates to a method of inducing



immunological response in a mammal which comprises delivering the IGS4 polypeptide via a vector directing expression of the IGS4 polynucleotide in vivo in order to induce such an immunological response to produce antibody to protect said animal from diseases. In particular the invention relates to a method for inducing an immunological response in a mammal which comprises inoculating the mammal with the IGS4 polypeptide, or a fragment thereof, if required together with a RAMP polypeptide, adequate to produce antibody and/or T cell immune response to protect said animal from disorders of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), disorders of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal muscle and/or of the thyroid, and/or also from lung diseases, immunological diseases and disorders of the genitourinary system.

A further aspect of the invention relates to an immunological/vaccine formulation (composition) which, when introduced into a mammalian host, induces an immunological response in that mammal to an IGS4 polypeptide wherein the composition comprises an IGS4 polypeptide or IGS4 gene. Such immunological/vaccine formulations (compositions) may be either therapeutic immunological/vaccine formulations or prophylactic immunological/vaccine formulations. The vaccine formulation may further comprise a suitable carrier. Since the IGS4 polypeptide may be broken down in the stomach, it is preferably administered parenterally (including subcutaneous, intramuscular, intravenous, intradermal etc. injection). Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the blood of the recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

### Screening Assays

The IGS4 polypeptide of the present invention may be employed in a screening process for compounds which bind the receptor and which activate (agonists) or inhibit activation of (antagonists) the receptor polypeptide of the present invention. Thus, polypeptides of the invention may also be used to assess the binding of small molecule substrates and ligands in, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. These substrates and ligands may be natural substrates and ligands or may be structural or functional mimetics.

IGS4 polypeptides are responsible for biological functions, including pathologies. Accordingly, it is desirable to find compounds and drugs which stimulate IGS4 on the one hand and which can inhibit the

function of IGS4 on the other hand. In general, agonists are employed for therapeutic and prophylactic purposes for such conditions as PNS, psychiatric and CNS disorders, including schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive disorder (OCD), post traumatic stress disorder (PTSD), phobia and panic, major depressive disorder, bipolar disorder, Parkinson's disease, general anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer disease/dementia and other neurodegenerative diseases, severe mental retardation, dyskinesias, Huntington's disease, Tourett's syndrome, tics, tremor, dystonia, spasms, anorexia, bulimia, stroke, addiction/dependency/craving, sleep disorder, epilepsy, migraine; attention deficit/hyperactivity disorder (ADHD); cardiovascular diseases, including heart failure, angina pectoris, arrhythmias, myocardial infarction, cardiac hypertrophy, hypotension, hypertension – e.g. essential hypertension, renal hypertension, or pulmonary hypertension, thrombosis, arteriosclerosis, cerebral vasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney disease – e.g. renal failure; dyslipidemias; obesity; emesis; gastrointestinal disorders, including irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), gastroesophageal reflux disease (GERD), motility disorders and conditions of delayed gastric emptying, such as post operative or diabetic gastroparesis, and diabetes, ulcers – e.g. gastric ulcer; diarrhoea; other diseases including osteoporosis; inflammations; infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; pain; cancers; chemotherapy induced injury; tumor invasion; immune disorders; urinary retention; asthma; allergies; arthritis; benign prostatic hypertrophy; endotoxin shock; sepsis; complication of diabetes mellitus; and gynaecological disorders. Antagonists may be employed for a variety of therapeutic and prophylactic purposes for such conditions as PNS, psychiatric and CNS disorders, including schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive disorder (OCD), post traumatic stress disorder (PTSD), phobia and panic, major depressive disorder, bipolar disorder, Parkinson's disease, general anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer disease/dementia and other neurodegenerative diseases, severe mental retardation, dyskinesias, Huntington's disease, Tourett's syndrome, tics, tremor, dystonia, spasms, anorexia, bulimia, stroke, addiction/dependency/craving, sleep disorder, epilepsy, migraine; attention deficit/hyperactivity disorder (ADHD); cardiovascular diseases, including heart failure, angina pectoris, arrhythmias, myocardial infarction, cardiac hypertrophy, hypotension, hypertension – e.g. essential hypertension, renal hypertension, or pulmonary hypertension, thrombosis, arteriosclerosis, cerebral vasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney disease – e.g. renal failure; dyslipidemias; obesity; emesis; gastrointestinal disorders, including irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), gastroesophageal reflux disease (GERD), motility disorders and conditions of delayed gastric emptying, such as post operative or diabetic gastroparesis, and diabetes, ulcers – e.g. gastric ulcer; diarrhoea; other diseases including osteoporosis; inflammations; infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; pain; cancers; chemotherapy induced injury; tumor invasion; immune disorders; urinary retention; asthma; allergies; arthritis; benign prostatic hypertrophy; endotoxin shock; sepsis; complication of diabetes mellitus; and

gynaecological disorders. Particularly, the present invention may be employed in a screening process for compounds which bind the receptor and which activate (agonists) or inhibit activation of (antagonists) the IGS4 neuromedin receptor protein, preferably the mammalian IGS4 neuromedin receptor protein, said protein exhibiting high affinity binding for neuromedin U, preferably for neuromedin U-8, for neuromedin U-23 and/or for neuromedin U-25. These screening assays are particularly suitable for screening compounds which are effective with regard to disorders of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), disorders of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal muscle and/or of the thyroid, and/or also to lung diseases, immunological diseases and disorders of the genitourinary system.

In general, such screening procedures involve producing appropriate cells, which express the receptor polypeptide of the present invention on the surface thereof and, if essential co-expression of RAMP's at the surface thereof. Such cells include cells from mammals, yeast, *Drosophila* or *E. coli*. Cells expressing the receptor (or cell membrane containing the expressed receptor) are then contacted with a test compound to observe binding, or stimulation or inhibition of a functional response.

One screening technique includes the use of cells which express the receptor of this invention (for example, transfected CHO cells) in a system which measures extracellular pH, intracellular pH, or intracellular calcium changes caused by receptor activation. In this technique, compounds may be contacted with cells expressing the receptor polypeptide of the present invention. A second messenger response, e.g., signal transduction, pH changes, or changes in calcium level, is then measured to determine whether the potential compound activates or inhibits the receptor.

Another method involves screening for receptor inhibitors by determining modulation of a receptor-mediated signal, such as cAMP accumulation and/or adenylate cyclase activity. Such a method involves transfecting an eukaryotic cell with the receptor of this invention to express the receptor on the cell surface. The cell is then exposed to an agonist to the receptor of this invention in the presence of a potential antagonist. If the potential antagonist binds the receptor, and thus inhibits receptor binding, the agonist-mediated signal will be modulated.

Another method for detecting agonists or antagonists for the receptor of the present invention is the yeast-based technology as described in U.S. Patent 5,482,835, incorporated by reference herein.

The assays may simply test binding of a candidate compound wherein adherence to the cells bearing the receptor is detected by means of a label directly or indirectly associated with the candidate compound or in an assay involving competition with a labeled competitor. Further, these assays may test whether the candidate compound results in a signal generated by activation of the receptor, using detection systems appropriate to the cells bearing the receptor at their surfaces. Inhibitors of activation

are generally assayed in the presence of a known agonist and the effect on activation by the agonist by the presence of the candidate compound is observed.

Thus candidate compounds may be screened which show ligand binding to the IGS4 receptors of the present invention. In the context of the present invention the term "ligand binding" is understood as to describe compounds with affinity to the IGS4 receptors showing log EC<sub>50</sub> values of at least below -6.00 (approx. 660 nM), preferably log EC<sub>50</sub> below -7.00 (approx. 55 nM), more preferably log EC<sub>50</sub> below -9.00 (approx. 500 pM to 1.2 nM), and most preferably log EC<sub>50</sub> below -10.00 (approx. 50-100 pM).

Thus in one aspect the invention concerns a method of determining whether a substance is a potential ligand of IGS4 receptor comprising

(a) contacting cells expressing one of the IGS4 neuromedin receptors defined supra or one of the receptors of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8, or contacting a receptor membrane preparation comprising one of said IGS4 neuromedin receptors defined supra or one of the receptors of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8 with labeled neuromedin U in the presence and in the absence of the substance; and

(b) measuring the binding of neuromedin U to IGS4.

Further, the assays may simply comprise the steps of mixing a candidate compound with a solution containing an IGS4 polypeptide to form a mixture, measuring the IGS4 activity in the mixture, and comparing the IGS4 activity of the mixture to a standard.

The IGS4 cDNA, protein and antibodies to the protein may also be used to configure assays for detecting the effect of added compounds on the production of IGS4 mRNA and protein in cells. For example, an ELISA may be constructed for measuring secreted or cell associated levels of IGS4 protein using monoclonal and polyclonal antibodies by standard methods known in the art, and this can be used to discover agents which may inhibit or enhance the production of IGS4 (also called antagonist or agonist, respectively) from suitably manipulated cells or tissues. Standard methods for conducting screening assays are well known in the art.

Examples of potential IGS4 antagonists include antibodies or, in some cases, oligonucleotides or proteins which are closely related to the ligand of the IGS4, e.g., a fragment of the ligand, or small molecules which bind to the receptor but do not elicit a response, so that the activity of the receptor is prevented.

Thus in another aspect, the present invention relates to a screening kit for identifying agonists, antagonists, ligands, receptors, substrates, enzymes, etc. for IGS4 polypeptides; or compounds which decrease, increase and/or otherwise enhance the production of IGS4 polypeptides, which comprises:

- (a) an IGS4 polypeptide, preferably that of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8;
- (b) a recombinant cell expressing an IGS4 polypeptide, preferably that of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8;
- 5 (c) a cell membrane expressing an IGS4 polypeptide; preferably that of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8; or
- (d) antibody to an IGS4 polypeptide, preferably that of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component.

### 10 Prophylactic and Therapeutic Methods

This invention provides methods of treating abnormal conditions related to both an excess of and insufficient amounts of IGS4 activity.

15 If the activity of IGS4 is in excess, several approaches are available. One approach comprises administering to a subject an inhibitor compound (antagonist) as hereinabove described along with a pharmaceutically acceptable carrier in an amount effective to inhibit activation by blocking binding of ligands to the IGS4, or by inhibiting interaction with a RAMP polypeptide or a second signal, and thereby  
20 alleviating the abnormal condition.

In another approach, soluble forms of IGS4 polypeptides still capable of binding the ligand in competition with endogenous IGS4 may be administered. Typical embodiments of such competitors comprise fragments of the IGS4 polypeptide.

25 In still another approach, expression of the gene encoding endogenous IGS4 can be inhibited using expression-blocking techniques. Known such techniques involve the use of antisense sequences, either internally generated or separately administered. See, for example, O'Connor, J Neurochem (1991) 56:560 in Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca  
30 Raton, Florida USA (1988). Alternatively, oligonucleotides, which form triple helices with the gene, can be supplied. See, for example, Lee et al., Nucleic Acids Res (1979) 6:3073; Cooney et al., Science (1988) 241:456; Dervan et al, Science (1991) 251:1360. These oligomers can be administered per se or the relevant oligomers can be expressed in vivo. Synthetic antisense or triplex oligonucleotides may comprise modified bases or modified backbones. Examples of the latter include methylphosphonate,  
35 phosphorothioate or peptide nucleic acid backbones. Such backbones are incorporated in the antisense or triplex oligonucleotide in order to provide protection from degradation by nucleases and are well known in the art. Antisense and triplex molecules synthesized with these or other modified backbones also form part of the present invention.

In addition, expression of the IGS1 polypeptide may be prevented by using ribozymes specific to the IGS1 mRNA sequence. Ribozymes are catalytically active RNAs that can be natural or synthetic (see for example Usman, N, et al., Curr. Opin. Struct. Biol (1996) 6(4), 527-33.) Synthetic ribozymes can be designed to specifically cleave IGS1 mRNAs at selected positions thereby preventing translation of the IGS1 mRNAs into functional polypeptide. Ribozymes may be synthesized with a natural ribose phosphate backbone and natural bases, as normally found in RNA molecules. Alternatively the ribozymes may be synthesized with non-natural backbones to provide protection from ribonuclease degradation, for example, 2'-O-methyl RNA, and may contain modified bases.

For treating abnormal conditions related to an under-expression of IGS4 and its activity, several approaches are also available. One approach comprises administering to a subject a therapeutically effective amount of a compound which activates IGS4, i.e., an agonist as described above, in combination with a pharmaceutically acceptable carrier, to thereby alleviate the abnormal condition. Alternatively, gene therapy may be employed to effect the endogenous production of IGS4 by the relevant cells in the subject. For example, a polynucleotide of the invention may be engineered for expression in a replication defective retroviral vector, as discussed above. The retroviral expression construct may then be isolated and introduced into a packaging cell transduced with a retroviral plasmid vector containing RNA encoding a polypeptide of the present invention such that the packaging cell now produces infectious viral particles containing the gene of interest. These producer cells may be administered to a subject for engineering cells in vivo and expression of the polypeptide in vivo. For overview of gene therapy, see Chapter 20, Gene Therapy and other Molecular Genetic-based Therapeutic Approaches, (and references cited therein) in Human Molecular Genetics, Strachan T. and Read A.P., BIOS Scientific Publishers Ltd (1996).

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

#### **Formulation and Administration**

Peptides, such as the soluble form of IGS4 polypeptides, and agonists and antagonist peptides or small molecules, may be formulated in combination with a suitable pharmaceutical carrier. Such formulations comprise a therapeutically effective amount of the polypeptide or compound, and a pharmaceutically acceptable carrier or excipient. Formulation should suit the mode of administration, and is well within the skill of the art. The invention further relates to pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention.

Polypeptides and other compounds of the present invention may be employed alone or in conjunction with other compounds, such as therapeutic compounds.

Preferred forms of systemic administration of the pharmaceutical compositions include injection, typically by intravenous injection. Other injection routes, such as subcutaneous, intramuscular, or intraperitoneal, can be used. Alternative means for systemic administration include transmucosal and transdermal administration using penetrants such as bile salts or fusidic acids or other detergents. In addition, if properly formulated in enteric or encapsulated formulations, oral administration may also be possible.

The dosage range required depends on the choice of peptide or compound, the route of administration, the nature of the formulation, the nature of the subject's condition, and the judgment of the attending practitioner. Suitable dosages are in the range of 0.1-100  $\mu\text{g/kg}$  of subject. Wide variations in the needed dosage, however, are to be expected in view of the variety of compounds available and the differing efficiencies of various routes of administration. For example, oral administration would be expected to require higher dosages than administration by intravenous injection. Variations in these dosage levels can be adjusted using standard empirical routines for optimization, as is well understood in the art.

Polypeptides used in treatment can also be generated endogenously in the subject, in treatment modalities often referred to as "gene therapy" as described above. Thus, for example, cells from a subject may be engineered with a polynucleotide, such as a DNA or RNA, to encode a polypeptide *ex vivo*, and for example, by the use of a retroviral plasmid vector. The cells are then introduced into the subject.

The following examples are only intended to further illustrate the invention in more detail, and therefore these examples are not deemed to restrict the scope of the invention in any way.



**EXAMPLE 1. THE CLONING OF CDNA ENCODING A NOVEL G PROTEIN-COUPLED RECEPTOR.****Example 1a. Homology PCR cloning of a genomic fragment encoding a novel G-protein coupled receptor (GPCR).**

5 A PCR based homology cloning strategy was used to isolate partial genomic DNA sequences encoding novel G-protein coupled receptors. Forward (F22) and reverse (R44 and R46) degenerate PCR primers were designed in conserved areas of the neurotensin receptor gene family (Vita N. et al. [1993] Febs Lett. 317, 139-142; Vita N. et al. [1998] Eur. J. Pharmacol. 360, 265-272) within  
10 transmembrane domains 1 (TM1) and 3 (TM3) and at the boundary between TM3 and intracellular loop 2 (I2):

F22 (TM1):

5'-CTCATCTTCGCGGTGGGC(A or G)C(A,C,G or T)G(C or T)(A,C,G or T)GG-3' (SEQ ID NO: 13)

R44 (TM3/I2):

5'-GGCCAGGCAGCGCTCCGCGCT(C or Inosine)A(A or G)(A,C,G or T)C(C or T)(A,C,G or T)GC(A,G or T)-3' (SEQ ID NO: 14)

R46 (TM3):

5'-GAA(A or G)TA(A or G)TAGCC(A or G)CG(A or G)CAGCC(A or T)-3' (SEQ ID NO: 15)

In order to suppress amplification of known members of the neurotensin receptor family, the 3' ultimate nucleotide position of primer R44 was chosen in such a way that is was not complementary to  
25 the corresponding position of both NTR1 and NTR2 cDNA. The primary PCR reaction was carried out in a 60µl volume and contained 100ng human genomic DNA (Clontech), 6 µl GeneAmp™ 10 x PCR buffer II (100mM Tris-HCl pH 8.3; 500 mM KCl, Perkin Elmer), 3.6 µl 25 mM MgCl<sub>2</sub>, 0.36 µl dNTPs (25mM of each dNTP), 1.5 units AmpliTaq-Gold™ polymerase (Perkin Elmer) and 30 pmoles of each of the degenerated forward (F22) and reverse primer (R44). Reaction tubes were heated at 95°C for 10 min  
30 and then subjected to 35 cycles of denaturation (95°C, 1 min), annealing (55°C, 2 min) and extension (72°C, 3min). Finally reaction tubes were heated for 10 min at 72°C.

For the semi-nested PCR reaction 1 µl of a 1/50 dilution of the primary PCR reaction was used as a template using the degenerate forward and reverse primers F22 and R46 respectively. The semi-nested PCR reaction was carried out under the same conditions as the primary PCR reaction.

35 Semi-nested PCR reaction products were size fractionated on an agarose gel and stained with ethidium bromide. Although a fragment of ± 220 bp was expected, only a fragment of ± 120 bp was visible. This fragment was purified from gel using the Qiaex-II™ purification kit (Qiagen) and ligated into the pGEM-T plasmid according to the procedure recommended by the supplier (pGEM-T kit, Promega). The recombinant plasmids thus produced were used to transform competent E. coli SURE™ 2 bacteria  
40 (Stratagene). Transformed cells were plated on LB agar plates containing ampicillin (100 µg/ml), IPTG (0.5 mM) and X-gal (50 µg/ml). Plasmid DNA was purified from mini-cultures of individual colonies using

a Qiagen-tip 20 miniprep kit (Qiagen). DNA sequencing reactions were carried out on the purified plasmid DNA with the ABI Prism™ BigDye™ Terminator Cycle Sequencing Ready Reaction kit (PE-ABI), using insert-flanking primers.

5

**Table 7: Overview of oligo primers used.**

SEQ ID NO: 13	F22: 5'-CTCATCTTCGCGGTGGGC(A or G)C(A,C,G or T)G(C or T)(A,C,G or T)GG-3'
SEQ ID NO: 14	R44: 5'-GGCCAGGCAGCGCTCCGCGCT(C or Inosine)A(A or G)(A,C,G or T)C(C or T)(A,C,G or T)GC(A,G or T)-3'
SEQ ID NO: 15	R46: 5'-GAA(A or G)TA(A or G)TAGCC(A or G)CG(A or G)CAGCC(A or T)-3'
SEQ ID NO: 16	AP1: 5'-CCATCCTAATACGACTCACTATAGGGC-3'
SEQ ID NO: 17	AP2: 5'-ACTCACTATAGGGCTCGAGCGGC-3'
SEQ ID NO: 18	IGS4R1: 5'GGATCCCAAATAAGAAAGGGTAGTTGC-3'
SEQ ID NO: 19	IGS4R2: 5'AAAGGGTAGTTGCGCCACATCTCATAGAC-3'
SEQ ID NO: 20	IGS4F5: 5'AGGTCTATGAGATGTGGCGCAACTACCCT-3'
SEQ ID NO: 21	IGS4F6: 5'ATGTGGCGCAACTACCCTTTCTTATTTGGG-3'
SEQ ID NO: 22	R74: 5'-CGGAAGTTGGCGGACACG(A or G)(A,C or G)(A or G)TT(A or G)TA-3'
SEQ ID NO: 23	IGS4F7: 5'-GCTCAGCTTGAAACAGAGCCTCGTACC-3'
SEQ ID NO: 24	IGS4F8: 5'-CCATGTGGATCTACAATTCATCATCC-3'
SEQ ID NO: 25	IGS4F9: 5'-AAGACAAATCTCTTGAGGCAGATGAAGGG-3'
SEQ ID NO: 26	IGS4F10: 5'-GATGCTGTTTGTCTTGGTCTTAGTGTTTGC-3'
SEQ ID NO: 27	IGS4R5: 5'-GGATGATGAAATTGTAGATCCACATGGGC-3'
SEQ ID NO: 28	IGS4R6: 5'-TGTGGAGAAGTCTCTCAAAGTGTGG-3'
SEQ ID NO: 29	IGS4R7: 5'-TAGTAGGAGTGACAGCCTGACTCGGAACG-3'
SEQ ID NO: 30	IGS4R8: 5'-AACGTAGATGACTCAGGACGAACCATTTCC-3'
SEQ ID NO: 31	IGS4F11: 5'-TCGTACCAGGGGAGGCTCAGGC-3'

Sequencing reaction products were purified via EtOH/NaOAc precipitation and analyzed on an ABI 377 automated sequencer.

Sequence analysis of the insert of clone HNT1552 showed that it potentially encoded part of a novel member of the GPCR family. We refer to this novel GPCR sequence as IGS4.

#### **Example 1b. Cloning of cDNA fragments containing the complete IGS4 coding sequence.**

The complete coding sequence of IGS4 cDNA was obtained via both RACE analysis (rapid amplification of cDNA ends) and RT-PCR amplification. 5'- and 3' RACE PCR reactions were performed on Marathon-Ready™ cDNA from human brain or testis (Clontech n° 7400-1 and 7414-1 respectively), using the adaptor primers 1 and 2 (AP1: SEQ ID NO: 16 ; AP2: SEQ ID NO: 17) provided with the

Marathon™ cDNA amplification kit (Clontech K1802-1) and IGS4 specific primers. PCR RACE reactions were performed according to the instructions of the Marathon-Ready™ cDNA user manual provided by Clontech. RACE products were separated on agarose gel, visualized with ethidium bromide and blotted onto Hybond N<sup>+</sup> membranes. Blots were prehybridized at 65°C for 2 h in modified Church buffer (0.5M phosphate, 7% SDS, 10 mM EDTA) and then hybridised overnight at 65°C in the same buffer containing 2 x 10<sup>6</sup> cpm / ml of a <sup>32</sup>P-labelled IGS4 cDNA probe. IGS4 cDNA probes were radiolabelled via random primed incorporation of [ $\alpha$ -<sup>32</sup>P]dCTP to a specific activity of > 10<sup>9</sup> cpm/ $\mu$ g using the Prime-It II kit™ (Stratagene) according to the instructions provided by the supplier. Hybridized blots were washed at high stringency (2 x 30 min at room temperature in 2 x SSC/ 0.1% SDS, followed by 2 washes of 40 min at 65°C in 0.1 x SSC, 0.1% SDS) and autoradiographed overnight. Hybridizing fragments were purified from a preparative gel, cloned into the pGEM-T vector and sequenced as described above.

An initial round of semi-nested 5' RACE analysis on human brain cDNA using the IGS4 specific primers IGS4R1 (SEQ ID NO: 18) and IGS4R2 (SEQ ID NO: 19)(designed on the DNA sequence of clone HNT1552) yielded clones HNT1886 and HNT1887 (Fig.1). These clones extended the IGS4 cDNA sequence upstream up to and beyond the putative start of translation codon. Likewise an initial round of 3' RACE analysis on human brain cDNA using IGS4 specific primers IGS4F5 (SEQ ID NO: 20) and IGS4F6 (SEQ ID NO: 21) yielded clones HNT1874-1878 and HNT1902-1903 (Fig.1). These clones extended the known IGS4 cDNA at the 3' end.

All sequences obtained at this point were assembled into a single contig which contained a long open reading frame, encoding part of a novel protein that was most similar to human orphan receptor FM-3 (Tan et al., Genomics 52, 223-229 [1998], GenBank accession n° AF044600 and AF044601). To investigate the RNA expression profile of IGS4, a Master Blot™ membrane (Clontech cat n° 7770-1) containing RNA from different human tissues was hybridized to the <sup>32</sup>P-labelled insert of clone HNT1903 under the conditions recommended by the supplier. The strongest hybridization was obtained with testis RNA whereas much weaker signals were obtained in prostate, stomach, spinal cord, hippocampus, medulla oblongata, thyroid gland, thymus, lung and trachea.

Since the contig sequence did not yet contain the complete IGS4 coding sequence we set up an RT-PCR homology cloning experiment on human total brain RNA using IGS4 specific primer IGS4F6 (SEQ ID NO: 21) and a degenerated primer (R74, SEQ ID NO: 22), which was designed in a conserved area (at the TM7/C-terminal intracellular part) of the GPCR subfamily composed of the neurotensin receptors 1 and 2, the growth hormone secretagogue receptor (Howard A.D. et al.[1996] Science 273, 974-977) and the orphan GPCR FM-3 and GPR38 (McKee K.K. et al.[1997] Genomics 46, 426-434). RT-PCR reactions were carried out in a 50  $\mu$ l volume on 500 ng total RNA from human brain using the Titan™ One Tube RT-PCR System (Boehringer catalogue n° 1,888,382) according to the recommendations of the supplier. Briefly, RT-PCR conditions were as follows: reverse transcription for 45 min at 55°C; 2 min denaturation at 94°C, followed by a touch-down PCR reaction of 20 cycles (30 sec denaturation at 94°C, 30 sec annealing at 60°C [-0.25°C/cycle] and 2 min extension at 68°C) and an additional round of 30 PCR cycles (30 sec denaturation at 94°C, 30 sec annealing at 55°C and 3 min [+ 5 sec/cycle] extension at 68°C). This was concluded with an extra extension step of 7 min at 68°C.

Reaction products were analyzed via Southern blotting using the radiolabelled insert of clone HNT1903. A fragment of  $\pm 690$  bp that hybridized to the probe was purified from the gel (QiaexII™, Qiagen) and cloned into the pGEM-T vector yielding clones HNT2210-2212. Sequence analysis of these clones allowed to extend the existing IGS4 cDNA contig in the 3' direction.

5 Since the extended IGS4 cDNA contig still did not yet contain a translational stop codon, additional IGS4 specific 3' RACE primers were designed (IGS4F7-10, SEQ ID NO: 23-26)). Nested or semi-nested 3' RACE reactions were carried out on Marathon Ready™ cDNA from human testis (Clontech 7414-1). IGS4 specific bands (as assessed via Southern blot analysis using an IGS4 specific probe) were cloned into pGEM-T. This yielded clones HNT2289-90 (AP1/IGS4F5->AP2/IGS4F9),  
 10 HNT2293-2295 (AP1/IGS4F6->AP2/IGS4F9), HNT2296-2297 (AP1/IGS4F7->AP2/IGS4F9), HNT2308-2310 (AP1/IGS4F8->AP2/IGS4F10) HNT2253 (AP1/IGS4F7->AP1/IGS4F5). An additional 5' RACE PCR reaction carried out on testis Marathon Ready™ cDNA yielded clones HNT2279-2281 (AP2/IGS4R6->AP2/IGS4R5). (note: AP1/IGS4F5->AP2/IGS4F9 e.g. indicates that clones were generated from an IGS4 specific fragment obtained after the primary RACE PCR reaction [using primer pair AP1/IGS4F5] was nested with primer pair AP2/IGS4F9).

15 Sequence analysis of these clones allowed to extend the existing IGS4 cDNA contig further in the 3' direction although the end of the IGS4 coding sequence was not yet been reached. A computer-assisted homology search (Blastn; Altschul S.F. et al., Nucleic Acids Res. (1997) 25:3389-3402) of the IGS4 contig DNA sequence against the expressed sequence tag (EST) database (dbest) showed the  
 20 presence of an EST sequence (accession n° N45474) which overlapped with the 3' end of the IGS4 contig (near 100 % identity in the overlap area). EST N45474 further extended the IGS4 DNA contig at the 3' end into a translational stop codon and into the 3' untranslated region (3'-UTR). In addition another set of ESTs was identified which all covered the 3'-UTR of the IGS4 mRNA (Fig.2). Additional IGS4 specific primers (IGS4R7-8, SEQ ID NO: 29-30)) were designed within the 3'-UTR of these ESTs.

25 Primary PCR reactions were carried out on Marathon Ready™ cDNA from human testis using various combinations of the IGS4F7 (SEQ ID NO: 23), IGS4F11 (SEQ ID NO: 31) and IGS4R7-8 (SEQ ID NO: 29-30) primers. PCR tubes were heated for 2 min at 95°C and then subjected to 35 cycles of denaturation (95°C, 30 sec), annealing (65°C, 30 sec) and extension (72°C, 1 min 30 sec). Finally the reactions tubes were heated at 72°C for 10 min. Nested PCR reactions were also carried out under the  
 30 same conditions. DNA fragments of  $\pm 1630$  bp were purified from gel and cloned into the pGEM-T vector. The following clones were obtained: HNT2311, HNT2312 and HNT2317 (IGS4F7/IGS4R7->IGS4F11/IGS4R8); HNT2313, HNT2324, HNT2326 and HNT2328 (IGS4F11->IGS4R8); HNT2314, HNT2315 and HNT2322 (IGS4F11->R7). Clone HNT2363 was obtained from a purified 1630 bp PCR fragment, that was amplified from human testis Marathon Ready™ cDNA using the IGS4F11/R7 primer pair under the following slightly modified conditions. After an initial denaturation of 2 min at 94°C, PCR tubes were subjected to 15 cycles of denaturation [15 sec, 94°C], annealing [30 sec, 65°C] and extension [2 min, 72°C] followed by another 20 cycles of denaturation [15 sec, 94°C], annealing [30 sec, 65°C] and extension [ 2 min, 72°C; +10sec/cycle]. There was a final extension step of 7 min at 72°C. Sequence analysis of these clones allowed to assemble an IGS4 cDNA consensus sequence (Fig.1).

Close inspection of all clones showed that they actually were of 2 sequence types, which differed at 5 nucleotide positions. These variant sequences correspond to a polymorphism within the human population. We refer to these different cDNA types as IGS4ADNA (SEQ ID NO: 1 and SEQ ID NO: 3) and IGS4BDNA (SEQ ID NO: 5 and SEQ ID NO: 7). The consensus sequence contained a long open reading frame that contained two in-frame start codons (positions 55-57 (SEQ ID NO: 1 and SEQ ID NO: 5) and 64-66 (SEQ ID NO: 3 and SEQ ID NO: 7) in IGS4ADNA and IGS4BDNA), predicting a protein of either 415 (SEQ ID NO: 2 and SEQ ID NO: 6) or 412 (SEQ ID NO: 4 and SEQ ID NO: 8) amino acids, which showed good homology to GPCR proteins. Hydropathy analysis (Kyte J. et al.[1982] J. Mol. Biol. 157: 105-132; Klein P. et al.[1985] Biochim. Biophys. Acta 815:468-476) of the protein also indicated the presence of 7 transmembrane domains. Since the first ATG initiator codon is within a weak "Kozak" translation initiation context and the second one is in a strong Kozak context, it is likely that the IGS4A/B protein starts at the second methionine and is 412 amino acids long (Kozak M. [1999] Gene 234, 187-208). However some (or even exclusive) initiation at the first ATG cannot be excluded. Among the five polymorphic nucleotides, four (positions 947, 999, 1202 and 1216 in IGS4A/BDNA) resulted in a switch in the encoded amino acid residue, whereas the fifth (pos 1381 in IGS4A/BDNA) was within the 3'-UTR. The respective predicted protein sequences are referred to as IGS4APROT (SEQ ID NO: 2 and SEQ ID NO: 4) and IGS4BPROT (SEQ ID NO: 6 and SEQ ID NO: 8). (note 1: the sequence of IGS4APROT and IGS4BPROT in this document is represented as the longest possible (415 amino acids) sequence but it is understood that the actual protein might be 3 amino acids shorter at the amino-terminus; for this reason the first 3 amino acids of IGS4APROT and IGS4BPROT in Table 4 and 5 have been bracketed) (note 2: In this document IGS4 refers to the IGS4 sequence in general, irrespective of the particular allelic type). Homology searches of the IGS4 protein sequence against public domain protein databanks showed best homology to the human orphan GPCR FM-3 (accession no O43664, Tan C.P., et al. Genomics (1998) 52: 223-229; 46% identity in IGS4A amino acid residues 26-342).

Homology searches of DNA databanks with the IGS4 cDNA sequence yielded a number of entries which were also derived from the IGS4 gene locus (Fig.2 for overview):

- 10 EST sequence entries (accession nrs W61169, AI432384, W61131, AI023570, F01358, F03770, Z38158, R40869, R37725, H11333), 2 STS (sequence tagged sites) (accession nrs G20615 and G05725) and one genomic sequence (accession nr AQ078563) were discovered which were all derived from the 3'-UTR of IGS4 cDNA.
- EST accession n° N45474 encoded the 3' end of the IGS4 coding sequence and part of the 3' UTR (cfr supra).
- A 'working draft' high throughput genomic sequence (accession nr AC008571, version AC008571.1, deposited 3 AUG 1999), which consisted of 42 unordered contigs assembled in an arbitrary order was discovered in which we detected the entire IGS4 cDNA sequence in 4 separate areas. These areas most likely correspond to the different IGS4 exons as they were flanked by canonical splice donor and acceptor sequences. On the basis of this analysis the position of the different exons in the IGS4ADNA (or IGS4BDNA) sequence can be defined as follows: exon1 (1-780), exon 2 (781-865), exon 3 (866-991) and exon 4 (992-1658). The AC008571 genomic sequence is of the IGS4A

allelic type.

- 6 overlapping EST entries (accession nrs H11359, R13890, R13353, F07531, F05108, F05107) were discovered of which the assembled DNA sequence overlapped at its 3' end with IGS4 exon2 and the beginning of exon 3. However the DNA sequence upstream of exon 2 was completely different from IGS4 exon1. Probably these six EST's are derived from transcripts which originated from an alternative promoter.
- Finally 2 genomic sequence entries (accession nrs AQ019411 and AQ015065) were discovered which encoded exon 2.

Among the many IGS4 cDNA clones that we isolated in the different experiments described above, we also discovered a number of clones that contained a 64 bp deletion (pos 866-929 in IGS4ADNA) (besides a number of clones derived from unspliced [or partially spliced] transcripts). So far we only discovered truncated transcripts of the polymorphic type A. We refer to this splice variant cDNA sequence as IGS4A-64DNA (SEQ ID NO: 9 and SEQ ID NO: 11). Since this deletion occurs exactly at the exon 2/exon 3 boundary and since the last 2 nucleotides of the deleted fragment are "AG", it is likely that this deletion represents an alternative splicing event in which the "AG" within exon 3 served as a splice acceptor. The IGS4A reading frame encoded by the splice variant is frameshifted beyond the deletion point. The encoded (truncated) protein of 296 amino acids is referred to as IGS4A-64PROT (SEQ ID NO: 10 and SEQ ID NO: 12). Hydropathy analysis of the IGS4A-64PROT sequence shows that this protein only contains 5 transmembrane domains (corresponding to TM domains 1-5 of IGS4APROT). This truncated receptor might have physiological relevance.

The bacterial strain harboring plasmid HNT2322 (containing the IGS4ADNA insert) was recloned after replating on LB agar plates containing 100 µg ampicillin/ml and deposited both in the Innogenetics N.V. strain list (ICCG4320) and at the "Centraalbureau voor Schimmelculturen (CBS)" in Baarn, The Netherlands (accession n° CBS102221). Plasmid DNA was prepared from the recloned isolate and the insert was resequenced and found to be identical to the IGS4ADNA sequence.

The bacterial strain harboring plasmid HNT2363 (containing the IGS4BDNA insert) was recloned after replating on LB agar plates containing 100 µg ampicillin/ml and deposited both in the Innogenetics N.V. strain list (ICCG4340) and at the "Centraalbureau voor Schimmelculturen (CBS)" in Baarn, The Netherlands (accession n° CBS102222). Plasmid DNA was prepared from the recloned isolate and the insert was resequenced and found to be identical to the IGS4BDNA sequence.

**EXAMPLE 2. SPECIFIC CHANGES IN INTRACELLULAR CALCIUM CONCENTRATIONS INDUCED IN CHOG 16-IGS4 CELLS BY NEUROMEDIN U.****Example 2a. Experimental Procedures: Method and Materials.****A. Method and Materials for IGS-4 transfected CHOG 16-cells.**

The following materials were used in the experiments: Vector containing IGS4-DNA sequence (IGS4-pcDNA3.1); SuperFect Transfection Reagent (Qiagen); Nut-Mix F12 (Gibco) with 10% FCS, 0.028mg/ml Gentamycin (Gibco); 0.22mg/ml Hygromycin (Gibco).

Materials used for clone selection: Nut-Mix F12 with 10% FCS; 0.028mg/ml Gentamycin; 0.22mg/ml Hygromycin and 0.55mg/ml Geneticin (Gibco).

The following method was applied: Transfection with SuperFect Transfection Reagent was carried out as described by the manufacturer (Qiagen). Cells were plated in 24-well plates to 50% confluence. Per well 0.6µg/µl plasmid-DNA with 1µl SuperFect Transfection Reagent was added. After 24 hours the medium was changed and transfected cell clones were selected by Geneticin-containing selection-medium. IGS4 expressing cell clones were characterized by RT-PCR and Northern Blot.

**B. Method and Materials for FLIPR-Assay.****Cell Preparation:**

For cell preparation the following materials were employed: plates: clear, flat-bottom, black well 96-well plates (Costar); Media: growth medium: Nut-Mix F-12 (HAM) with Glutamax (Gibco) supplemented with 10% fetal calf serum (Gibco); Incubator: 5% CO<sub>2</sub>, 37°C (Nuaire).

The method was performed as follows: Cells were seeded 24 hours or 48 hours prior to the experiment into black wall microplates. The cell density was 0.8x10<sup>4</sup> cells/well for 48 hour incubation and 2.2x10<sup>4</sup> cells/well for 24 hour incubation. All steps were done under sterile conditions.

**Dye loading:**

In order to observe changes in intracellular calcium levels, cells must be 'loaded' with a calcium-sensitive fluorescent dye. This dye, called FLUO-4 (Molecular Probes) is excited at 488nm, and emits light in the 500-560nm range, only if a complex with calcium is formed. The dye was used at 4µM final concentration. Pluronic acid was added to increase dye solubility and dye uptake into the cells. Probenicid, an anion exchange protein inhibitor, was added to the dye medium to increase dye retention in the cells.

The following materials were used:

- 2mM dye stock: 1mg Fluo-4 (Molecular Probes) solubilized in 443µl low-water DMSO (Sigma). Aliquots stored at -20.



- 20% pluronic acid solution: 400mg pluronic acid (Sigma) solubilized in 2ml low-water DMSO (Sigma) at 37°C. Stored at room temperature.
- Dye/pluronic acid mixture: Immediately before use, equal volumes of the dye stock and 20% pluronic acid were mixed. The dye and pluronic acid had a final concentration of 1mM and 10%, respectively.
- Probenicid, 250mM stock solution: 710mg probenicid (Sigma) solubilized in 5ml 1N NaOH and mixed with 5ml Hank's BSS without phenol red (Gibco) supplemented with 20mM HEPES.
- Loading-Buffer: 10.5ml Hank's BSS without phenol red (Gibco) supplemented with 20mM HEPES, 105µl probenicid, 210µl 1M HEPES.
- Wash-Buffer: Hank's BSS without phenol red (Gibco) supplemented with 20mM HEPES (Gibco) and 2.5mM probenicid.

The method was worked as follows: The 2mM stock of dye was mixed with an equal volume of 20% (w/v) pluronic acid immediately before adding to the loading-Buffer. The growth-medium was aspirated out of the well without disturbing the confluent cell layer. 100µl loading medium was dispensed into each well using a Multidrop (Labsystems). Cell were incubated in a 5% CO<sub>2</sub>, 37°C incubator for 30 minutes. In order to calculate the background fluorescence, some wells were not dye loaded. The background fluorescence in these wells results from autofluorescence of the cells. After dye loading, cell were washed three times with Wash-Buffer (automated Denley cell washer) to reduce the basal fluorescence to 20.000-25.000 counts above background. 100 l buffer was added and cell were incubated at 37°C till start of the experiment.

### C. Preparation of compound plates.

The peptides were prepared at 3µM (3x the final concentration) for initial screening. For concentration response curves peptide-solutions were prepared in concentration ranges from 30µM to 100nM. All peptides were diluted in buffer containing 0.1% BSA (Sigma).

The following materials were used: Peptides: porcine Neuromedin U25, rat Neuromedin U-23, porcine Neuromedin U-8 (Bachem); Dilutionbuffer: Hank's BSS without phenol red (Gibco) supplemented with 20mM HEPES (Gibco) and 0.1% BSA (Sigma); plates: clear, flat-bottom, 96-well plates (Costar).

### D. Assay.

The FLIPR setup parameters were set to 0.4 sec exposure length, filter 1, 50µl fluid addition, pipettor height at 125µl, Dispense Speed 40µl/sec without mixing.

### Example 2b. Results.

To identify the endogenous ligand for the orphan G protein coupled receptor (GPCR) IGS4, IGS4 (both forms IGS4A and IGS4B) was stably transfected in Chinese Hamster Ovary (CHO) cells. Since the G protein coupling mechanism of IGS4 was unknown, a specific CHO-cell strain was used. These CHO-

cells stable express the G-protein G 16 (CHOG 16, Molecular Devices), which is known as "universal adapter" for GPCRs (Milligan G., Marshall F. and Rees S. (1996),  $G\alpha_{16}$  as a universal G protein adapter: implications for agonist screening strategies. *TIPS* 17: 235-237).

The resulting CHOG 16-IGS4 cells were functionally screened on a Fluorometric Imaging Plate Reader (FLIPR) to measure mobilisation of intracellular calcium in response to putative peptide ligands.

At the concentration of 10nM neuromedin U-23 induced a large, transient and robust calcium-response. In contrast, CHOG 16 cells and CHOG 16 cells expressing another, unrelated orphan GPCR, did not respond to neuromedin U-23. The results of these experiments with IGS4B are shown in Fig. 4.

Furthermore, the concentration dependence of IGS4 activation by porcine and rat neuromedin U isoforms were investigated (for both forms IGS4A and IGS4B). In the range of  $10^{-6}$ - $10^{-12}$  M porcine neuromedin U-25, rat neuromedin U-23, porcine neuromedin U-8 induced specific IGS4-mediated calcium mobilisation in the FLIPR assay. All three Neuromedin U isoforms tested caused the same maximal activation of IGS4B with  $\text{LogE.C}_{50}$  values of  $-10.09 \pm 0.08$  (neuromedin U-8,  $n=4$ ; 80 pM),  $-10.61 \pm 0.08$  (neuromedin U-23,  $n=10$ ; 50 pm) and  $-9.14 \pm 0.09$  (neuromedin U-25,  $n=3$ ; 1.2 nM). Thus, all three peptides cause potent activation of in particular IGS4B, suggesting that neuromedin U is the natural agonist for this receptor. The results of these experiments with IGS4B are shown in Fig. 3a (neuromedin U-8), Fig. 3b (neuromedin U-23) and Fig. 3c (neuromedin U-25).

For the IGS4A receptor somewhat lower affinities were found, but still showing that the neuromedin U peptides are good ligands for IGS4 receptors in general. The  $\log EC_{50}$  values found for IGS4A were as follows; for neuromedin U-8:  $\log EC_{50} = -9.3 \pm 0.09$  ( $n=1$ ; 485 pM); for neuromedin U-23:  $\log EC_{50} = -7.27 \pm 0.16$  ( $n=6$ ; 53 nM); and for neuromedin U-25:  $\log EC_{50} = -6.18 \pm 0.14$  ( $n=3$ ; 658 nM).

The calcium mobilisation response seen following activation of IGS4 by neuromedin U suggests that this receptor is coupled to G proteins of the Gq/11 subfamily. In addition, basal levels of intracellular cAMP were not modulated by porcine neuromedin U-8 (1 and 10 $\mu$ M) in CHOG 16-IGS4 cells, suggesting that this receptor does not couple to G proteins of the Gs subfamilies (data not shown).

### EXAMPLE 3. IGS4 HYBRIDIZATION ON HUMAN MULTIPLE TISSUE EXPRESSION ARRAY (MTE™)

Human IGS4A DNA ( $\pm$  730 bp BamHI / HindIII insert from pGEMT-hIGS4A [ICCG #4320] ) was radiolabelled via random primed incorporation of [ $^{32}$ P]-dCTP to a specific activity of  $> 10^9$  cpm/ $\mu$ g using the Prime-It II kit™ (Stratagene). The labeled probe was purified from free label via Sephadex G-50 chromatography, denatured for 5 min. at 95°C and added to the ExpressHyb hybridization solution at a final concentration of  $1-1.5 \times 10^6$  cpm/ml. The human Multiple Tissue Expression (MTE™) Array (Clontech # 7775-1) was prehybridized and hybridized in ExpressHyb solution at 65°C for 30 min and overnight respectively according to the recommendations of the supplier.

The hybridized MTE™ array was washed 5 times for 20 min in 2 x SSC, 1% SDS at 65°C and then 2 times for 20 min at 55°C in 0.1 x SSC, 0.5% SDS. After the washes the array was autoradiographed via phosphorimaging (Cyclone Storage Phosphor System, Packard) (Fig.5). Hybridization data of the MTE™ array were analyzed quantitatively using the OptiQuant Image Analysis Software (Packard). Signal intensity of different spot positions containing RNA was corrected for the average background signal obtained from empty positions. The signal intensity obtained from the spot containing E. coli DNA was considered to represent a sample exhibiting no IGS4 expression. Samples with signal intensities below that of E. coli DNA were considered to be negative.

Hybridization signals for different tissues on the RNA array have been recalculated by subtracting each value with the hybridization signal observed for E. coli DNA (which is considered as the background signal). All tissues showing a lower hybridization signal are considered to be below background and to be IGS4 negative. Expression levels relative to that found in testis (100%) have been plotted and are provided in Fig.7.

#### EXAMPLE 4. TISSUE DISTRIBUTION OF IGS4 BY NORTHERN BLOT ANALYSIS

Human IGS4A DNA ( $\pm$  730 bp BamHI / HindIII insert from pGEMT-hIGS4A [ICCG #4320] ) was radiolabelled via random primed incorporation of [ $^{32}$ P]-dCTP to a specific activity of  $> 10^9$  cpm/ $\mu$ g using the Prime-It II kit™ (Stratagene). The labeled probe was purified from free label via Sephadex G-50 chromatography, denatured for 5 min. at 95°C and added to the ExpressHyb hybridization solution at a final concentration of  $1-1.5 \times 10^6$  cpm/ml. The human Northern blots ( Clontech #7760-1, #7759-1, #7767-1, #7755-1 and #7769-1) were prehybridized and hybridized in ExpressHyb solution at 65°C for 30 min and overnight respectively according to the recommendations of the supplier.

After hybridization Northern blots were washed 4 times 10 min at room temperature in 2 x SSC, 0.05 % SDS and then 2 times 40 min at 50°C in 0.1 x SSC, 0.1% SDS. After the washes the Northern blots were autoradiographed using phosphor storage plates (Cyclone Storage Phosphor System, Packard) and X-ray films. Results of Northern blots are shown in Fig.6.

The results of the Northern blot analysis appear to be largely consistent with those from the array hybridization (Example 3). The strongest signal (2.4 kb transcript) by far is found in testis. A weak 2.4 kb band was found in thymus, spinal cord, medulla, thyroid, thalamus, substantia nigra and a very weak band in corpus callosum, caudate nucleus and stomach. For some tissues no 2.4 kb band could be seen on Northern whereas a strong to moderate hybridization signal was observed on the MTE array (e.g. whole brain, cerebral cortex, lung, temporal and frontal lobe, amygdala, cerebellum, kidney and hippocampus).

**EXAMPLE 5. QUANTITATIVE RT-PCR ANALYSIS.**

IGS4 expression levels in different human tissues were also determined via real-time quantitative RT-PCR (Q-PCR) using the LightCycler™ instrument (Roche Diagnostics) and IGS4 specific TaqMan™ probes.

**Example 5a. Experimental procedures.****A. cDNA synthesis.**

Prior to reverse transcription 3 µg total RNA from the human total RNA panels I to V (Clontech # K4000-1 to K4004-1) was treated with 3U DNase I (Life Technologies # 18068-015) in a 30 µl reaction volume (20 mM Tris pH 8.3, 50 mM KCl, 2 mM KCl) for 15 min at room temperature to destroy possibly contaminating genomic DNA. The reaction was stopped by adding 3 µl 25 mM EDTA and heating for 10 min at 65°C. 2,6 µg of the DNase treated RNA was annealed with 1,3 µg oligo(dT) (Life Technologies # 18418-012) and subjected to reverse transcription using the Omniscript reverse transcriptase (Qiagen cat n° 205111) for 1 h at 37°C in a 52 µl reaction volume according to the protocol recommended by the supplier of the enzyme. The Omniscript reverse transcriptase was inactivated by heating at 93°C for 5 min.

**B. Q-PCR.**

Quantitative PCR reactions were carried out in a 20 µl reaction mixture, containing 1X TaqMan™ Universal PCR Mastermix (PE Applied Biosystems cat #4304437), 0.12 mg BSA/ml, 900 nM of IGS4 specific forward and reverse primers (IP14,963 and IP14,964), 250 nM of the IGS4 specific TaqMan™ probe (IP14,962) and either 1.6 µl (IGS4) or 0.16 µl (GAPDH: glyceraldehyde-3 phosphate dehydrogenase) of the cDNA synthesis reaction as template. To set up the IGS4 standard curve a dilution series (10<sup>7</sup> -10<sup>1</sup>copies/ reaction) of IGS4 plasmid ICCG 4320 was used whereas for the GAPDH standard curve a dilution series of the human brain cDNA synthesis reaction (0.16 µl, 0.016 and 0.0016 µl) was used as template. The 1X TaqMan™ Universal PCR Mastermix contained AmpliTaq Gold™ DNA polymerase, AmpErase™ UNG (uracil-N-glycosylase), dNTPs with dUTP, passive reference and optimized buffer components. IGS4 specific primers and TaqMan probe were designed using the Primer Express™ software (PE Applied Biosystems). Quantitative PCR reactions for human GAPDH were carried out under identical conditions as described for IGS4 except that GAPDH specific primers and TaqMan™ probe were used from the TaqMan™ GAPDH control reagents kit (PE Applied Biosystems cat n° 402869; sequence information not available from PE Applied Biosystems).

PCR reactions were carried out in glass capillary cuvettes in the LightCycler™ instrument. After an initial incubation at 50°C for 2 min to allow the AmpErase™ UNG reaction to proceed and activation of the AmpliTaq Gold DNA polymerase (95°C for 10 min), reaction mixtures were subjected to 40 cycles of denaturation (15 sec at 95°C) and annealing/extension (1 min at either 60 °C [GAPDH] or at 68°C

[IGS4]). Quantification of experimental samples was carried out using the LightCycler Software version 3.0. A good linear relationship was obtained between the amount of IGS4 plasmid and the release of reporter dye within the range of  $10^{-10}$  to  $10^{-7}$  IGS4 plasmid copies. We also obtained a linear standard curve with the GAPDH TaqMan<sup>TM</sup> probe using the serially diluted brain cDNA. Relative GAPDH expression levels were in the range of 0.4 to 10.2 % of that observed in skeletal muscle, which of all tissues tested had the highest GAPDH expression level. Relative IGS4 expression levels were expressed as a proportion of the level detected in spinal cord, which had the highest IGS4 expression of all tissues tested (Fig.8). We also plotted relative IGS4 expression levels after normalization for expression of the GAPDH house keeping gene (Fig.8).

#### Example 5b. Results.

Q-PCR using an IGS4 specific TaqMan probe showed that highest expression levels (without normalization for GAPDH) were found in spinal cord. IGS4 expression levels in spinal cord amounted to 11,467 copies mRNA / ng pA RNA (assuming 100 % efficiency of the cDNA synthesis reaction and assuming that pA RNA constitutes 2% of total RNA). High IGS4 expression levels were also found in brain (41 % of spinal cord levels), skeletal muscle (37%), cerebellum (31%), testis (19%) and in lung (12%) and heart (11%). Lower levels were found in fetal brain (5%), trachea (4%), prostate (2%) and thyroid (1.4%). After normalization for GAPDH expression, the relative IGS4 expression pattern remained largely unchanged with the exception of skeletal muscle, where the relative expression level dropped to 2% of that in spinal cord. As it is not clear whether normalization for GAPDH is a valid procedure (GAPDH expression levels can be expected to vary more or less in different cell/ tissue types) we prefer to focus on the non-normalized relative expression levels.

These Q-PCR data seem to be in line with expression data from RNA array (Example 3) and Northern blot (Example 4) hybridization experiments in the sense that testis, spinal cord and brain appear to be among the most prominent expression sites. However Q-PCR analysis additionally shows important expression in a number of other tissues, such as skeletal muscle, cerebellum, lung and heart.

The ligand neuromedin U has been proposed to be a neuropeptide or neuromodulator, without the knowledge of the specific receptor (Domin J., Ghatei M. A., Chohan P. and Bloom S. R. (1987), Peptides 8: 779-784). Our investigation shows, that IGS4 is a novel member of the neuromedin U-receptor family being expressed in CNS and PNS regions, the gastrointestinal, immunological, genitourinary and cardiovascular system, skeletal muscle, thyroid, and lung.

Table 8: Overview of the PCR oligonucleotide primers and TaqMan probe used in the IGS4 Q-PCR reactions.

SEQ ID NO: 32	IP 14,963	5'-CCTCTTCAGCCTGGCGGTCTCTG-3'
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SEQ ID NO: 33	IP 14,964	5'- GGAGGCGAAGCACACGGTCTCA-3'
SEQ ID NO: 34	IP 14,962	5'(FAM)-AGATGTGGCGCAACTACCCTTTCTTGTTCTGGGCC-(TAMRA)3'

All publications, including but not limited to patents and patent applications, cited in this specification are herein incorporated by reference as if each individual publication were specifically and individually indicated to be incorporated by reference herein as though fully set forth.

**The figures show:**

Fig.1 Schematic representation of the relative positions of the different cDNA clones that were isolated to generate the consensus IGS4 cDNA sequence. 5' and 3' RACE primers that were used are also indicated (IGS4R# and IGS4F# respectively) as well as the position of EST accession n° N45474. Primer IGS4R6 was located within intron 1. Some clones (e.g. HNT2311, HNT2312 and HNT2253) were only partially sequenced (only the part that was sequenced is indicated). CONSENSUS A and CONSENSUS B denote the consensus sequence of IGS4 allelic types A and B respectively. The nucleotide that was identified at each of the 4 polymorphic positions is indicated (shaded boxes) for each clone. "S" indicates a sequence ambiguity in clones HNT2211 and HNT2212 and means either "C" or "T". The coding area of IGS4A and IGS4B consensus sequences is indicated with "\*\*\*\*". As there were some remaining sequence ambiguities in the 5' end of the consensus sequence, the IGS4ADNA and IGS4BDNA sequences have only been taken from position 86 until the end

Fig.2 Schematic representation of the relative positions of different DNA database entries compared to the IGS4 cDNA sequence. The IGS4 cDNA sequence is indicated with the boxes (the position of the IGS4 coding sequences is indicated with the filled boxes). The relative position of IGS4 exons 1-4 is indicated above the IGS4 cDNA sequence ("=="). The parts of the genomic sequence AC008571 that encode exons 1->4 are indicated with AC008571a->d respectively. The position of these fragments within the AC008571 sequence are: AC008571a (13129-13908 of the reverse complement of AC008571), AC008571b (51676-51760 of AC008571), AC008571c (79978-80103 of the reverse complement of AC008571) and AC008571d (83060-83728 of the reverse complement of AC008571). G05725 and G20615 are STS (sequence tagged sequence) entries whereas F05107, F05108, F07531, R13353, R13890, H11359, N45474, W61169, AI432384, W61131, AI023570, F01358, F03770, Z38158, R40869, R37725, H11333 are EST entries. The parts of genomic clones AQ019411 and AQ015065 that contain IGS4 exon 2 are indicated with ":". The 5' part of EST sequences F05107, F05108, F07531, R13353, R13890 and H11359 which is totally different from the IGS4 cDNA sequence is indicated with "\*\*". AQ078563 is a genomic clone.

Fig.3 : IGS4 receptor activation by different Neuromedin U isoforms. CHOG 16-IGS4B cells were cultured in 96-well plates overnight and loaded with Fluo-4AM. The receptor mediated  $Ca^{2+}$  changes were measured with FLIPR (Molecular Devices). Maxima of the fluorescence change detected by the CCD camera were normalised to 1 and are depicted as counts.

Fig. 3a: results for neuromedin U-8;  
 Fig. 3b: results for neuromedin U-23;  
 Fig. 3c: results for neuromedin U-25.



Fig.4 Neuromedin U-23 induced intracellular  $\text{Ca}^{2+}$  mobilisation in CHO G 16-cells expressing IGS4B. Application of 10nM Neuromedin U-23 to the cell lines CHO G 16-IGS4, CHO G 16 and CHO G 16 transfected with an other orphan GPCR. Cells were cultured in 96-well plates overnight and loaded with Fluo-4AM. Receptor mediated intracellular  $\text{Ca}^{2+}$  changes were measured with FLIPR (Molecular Devices), depicted in counts detected by the CCD camera.

Fig. 5 Human multiple tissue expression array using a human IGS4 probe.

Fig. 6 Northern blot analysis using an IGS4 probe.

Fig. 7 IGS4 expression analysis (MTE blot).

Fig. 8 Relative expression levels of IGS4 mRNA as compared to the expression observed in spinal cord. Both non-normalized and GAPDH-normalized expression levels are shown.

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1	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
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1-2	line	25>
1-3	Identification of Deposit	
1-3-1	Name of depositary institution	Centraalbureau voor Schimmelcultures
1-3-2	Address of depositary institution	Oosterstraat 1, Postbus 273, NL-3740 AG Baarn, Netherlands
1-3-3	Date of deposit	24 September 1999 (24.09.1999)
1-3-4	Accession Number	CBS 102221
1-4	Additional Indications	none
1-5	Designated States for Which Indications are Made	all designated States
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2-3-1	Name of depositary institution	Centraalbureau voor Schimmelcultures
2-3-2	Address of depositary institution	Oosterstraat 1, Postbus 273, NL-3740 AG Baarn, Netherlands
2-3-3	Date of deposit	24 September 1999 (24.09.1999)
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**Claims**

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
  - a) a nucleotide sequence encoding the IGS4 polypeptide according to SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8;
  - b) a nucleotide sequence encoding the polypeptide encoded by the DNA insert contained in the deposit no. CBS102221 or the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands, in particular a nucleotide sequence comprising SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7;
  - c) a nucleotide sequence having at least 80 % (preferably at least 90%) sequence identity over its entire length to the nucleotide sequence of (a) or (b);
  - d) a nucleotide sequence which is complimentary to the nucleotide sequence of (a) or (b) or (c).
2. The polynucleotide of claim 1 wherein said polynucleotide comprises the nucleotide sequence contained in SEQ ID NO: 1 encoding the IGS4 polypeptide of SEQ ID NO: 2 or the nucleotide sequence contained in SEQ ID NO: 3 encoding the IGS4 polypeptide of SEQ ID NO: 4 or the nucleotide sequence contained in SEQ ID NO: 5 encoding the IGS4 polypeptide of SEQ ID NO: 6 or the nucleotide sequence contained in SEQ ID NO: 7 encoding the IGS4 polypeptide of SEQ ID NO: 8.
3. The polynucleotide of claim 1 wherein said polynucleotide comprises a nucleotide sequence that is at least 80% identical to that of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7 or to the sequence of the DNA insert contained in the deposit no. CBS102221 or the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands over its entire length.
4. The polynucleotide of claim 3 which is the polynucleotide of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7 or the DNA insert contained in the deposit no. CBS102221 or the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands.
5. The polynucleotide of claim 1-4 which is DNA or RNA.

6. An isolated nucleotide sequence encoding an IGS4 neuromedin receptor protein comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8, preferably a mammalian neuromedin receptor protein, said protein exhibiting high affinity binding for neuromedin U, preferably for neuromedin U-8, for neuromedin U-23 and/or for neuromedin U-25.
7. An isolated nucleotide sequence of claim 6 encoding an IGS4 neuromedin receptor protein comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8, said protein exhibiting expression in brain, skeletal muscle, cerebellum, testis, corpus callosum, spinal cord, substantia nigra, medulla, thalamus, caudate nucleus, pons, nucleus accumbens, fetal brain, stomach, heart, thyroid gland, lung, thymus, prostate and/or in trachea.
8. An isolated nucleotide sequence encoding an IGS4 neuromedin receptor protein comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8, preferably a mammalian neuromedin receptor protein, said protein exhibiting high affinity binding for neuromedin U, preferably for neuromedin U-8, for neuromedin U-23 and/or for neuromedin U-25, said protein exhibiting expression in brain, skeletal muscle, cerebellum, testis, corpus callosum, spinal cord, substantia nigra, medulla, thalamus, caudate nucleus, pons, nucleus accumbens, fetal brain, stomach, heart, thyroid gland, lung, thymus, prostate and/or in trachea, and said nucleotide sequence being selected from the group of nucleotide sequences as defined in the claims 1 to 5.
9. A DNA or RNA molecule comprising an expression vector, wherein said expression vector is capable of producing an IGS4 polypeptide comprising an amino acid sequence, which has at least 80% identity with the polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8 or with the polypeptide encoded by the DNA insert contained in the deposit no. CBS102221 or the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands, when said expression vector is present in a compatible host cell.
10. An isolated DNA or RNA molecule comprising an expression vector, wherein said expression vector is capable of producing an IGS4 neuromedin receptor protein comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ

ID NO:6 or SEQ ID NO:8, preferably a mammalian neuromedin receptor protein, said protein exhibiting high affinity binding for neuromedin U, preferably for neuromedin U-8, for neuromedin U-23 and/or for neuromedin U-25, and exhibiting expression in brain, skeletal muscle, cerebellum, testis, corpus callosum, spinal cord, substantia nigra, medulla, thalamus, caudate nucleus, pons, nucleus accumbens, fetal brain, stomach, heart, thyroid gland, lung, thymus, prostate and/or in trachea.

11. A host cell comprising the expression system of claim 9 or 10.
12. A host cell according to claim 11 which is a yeast cell.
13. A host cell according to claim 11 which is an animal cell.
14. IGS4 receptor membrane preparation derived from a cell according to claim 11-13.
15. A process for producing an IGS4 polypeptide comprising culturing a host of claim 11-13 under conditions sufficient for the production of said polypeptide and recovering the polypeptide from the culture.
16. A process for producing a cell which produces an IGS4 polypeptide comprising transforming or transfecting a host cell with the expression system of claim 9 or 10 such that the host cell, under appropriate culture conditions, produces an IGS4 polypeptide.
17. An IGS4 polypeptide comprising an amino acid sequence which is at least 80% identical to the amino acid sequence of SEQ ID NO: 2, SEQ NO: 4, SEQ NO: 6 or SEQ NO: 8 or to the polypeptide encoded by the DNA insert contained in the deposit no. CBS102221 or the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands over its entire length.
18. The polypeptide of claim 17 which comprises the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, SEQ NO: 6 or SEQ NO: 8 or the amino acid sequence encoded by the DNA insert contained in the deposit no. CBS102221 or the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands.

19. An isolated IGS4 neuromedin receptor protein comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8, preferably of a mammalian neuromedin receptor protein, said protein exhibiting high affinity binding for neuromedin U, preferably for neuromedin U-8, for neuromedin U-23 and/or for neuromedin U-25.
20. An isolated IGS4 neuromedin receptor protein of claim 19 comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8, said protein exhibiting expression in brain, skeletal muscle, cerebellum, testis, corpus callosum, spinal cord, substantia nigra, medulla, thalamus, caudate nucleus, pons, nucleus accumbens, fetal brain, stomach, heart, thyroid gland, lung, thymus, prostate and/or in trachea.
21. An isolated IGS4 neuromedin receptor protein comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8, preferably a mammalian neuromedin receptor protein, said protein exhibiting high affinity binding for neuromedin U, preferably for neuromedin U-8, for neuromedin U-23 and/or for neuromedin U-25, said protein exhibiting expression in brain, skeletal muscle, cerebellum, testis, corpus callosum, spinal cord, substantia nigra, medulla, thalamus, caudate nucleus, pons, nucleus accumbens, fetal brain, stomach, heart, thyroid gland, lung, thymus, prostate and/or in trachea, and said amino acid sequence being selected from the group of amino acid sequence as defined in the claims 17-18.
22. An antibody immunospecific for the IGS4 polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8 of claim 17-21.
23. Use of:
  - (a) a therapeutically effective amount of an agonist to the IGS4 neuromedin receptor polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8 of claim 17-21; and/or
  - (b) an isolated polynucleotide comprising a nucleotide sequence that has at least 80% identity to a nucleotide sequence encoding the IGS4 polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, SEQ NO: 6 or SEQ NO: 8 or the polypeptide encoded by



the DNA insert contained in the deposit no. CBS102221 or the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands over its entire length; or a nucleotide sequence complementary to one of said nucleotide sequences in a form so as to effect production of said receptor activity in vivo; and/or

(c) an isolated polynucleotide comprising a nucleotide sequence that encodes an IGS4 neuromedin receptor protein comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8, preferably a mammalian IGS4 neuromedin receptor protein, said protein exhibiting high affinity binding for neuromedin U, preferably for neuromedin U-8, for neuromedin U-23 and/or for neuromedin U-25,

for the preparation of a medicament for the treatment of a subject suffering from a disease related to expression or activity of the IGS4 neuromedin receptor polypeptide, in need of enhanced activity or expression of IGS4 polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8 of claim 17-21.

24. Use of:

(a) a therapeutically effective amount of an antagonist to the IGS4 neuromedin receptor polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8 of claim 17-21; and/or

(b) a nucleic acid molecule that inhibits the expression of the nucleotide sequence encoding the IGS4 neuromedin receptor polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8 of claim 17-21; and/or

(c) a therapeutically effective amount of a polypeptide that competes with the IGS4 neuromedin receptor polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8 of claim 17-21 for its ligand,

for the preparation of a medicament for the treatment of a subject suffering from a disease related to expression or activity of the IGS4 neuromedin receptor polypeptide, having need to inhibit activity or expression of IGS4 polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8 of claim 17-21.

25. A process for diagnosing a disease or a susceptibility to a disease in a subject related to expression or activity of the IGS4 neuromedin receptor polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8 of claim 17-21 in a subject, comprising:
- (a) determining the presence or absence of a mutation in the nucleotide sequence encoding said IGS4 polypeptide in the genome of said subject in a sample derived from said subject; and/or
  - (b) analyzing for the presence or amount of said IGS4 polypeptide expression in a sample derived from said subject.
26. A method for identifying agonists to the IGS4 polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8 of claim 17-21, comprising:
- (a) contacting a cell which produces said IGS4 polypeptide with a test compound; and
  - (b) determining whether the test compound effects a signal generated by activation of the IGS4 polypeptide.
27. An agonist identified by the method of claim 26.
28. A method for identifying agonists to the IGS4 neuromedin receptor protein comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8, preferably to the mammalian IGS4 neuromedin receptor protein, said protein exhibiting high affinity binding for neuromedin U, preferably for neuromedin U-8, for neuromedin U-23 and/or for neuromedin U-25, comprising:
- (a) contacting a cell which produces said IGS4 neuromedin receptor protein with a test compound; and
  - (b) determining whether the test compound effects a signal generated by activation of the IGS4 neuromedin receptor protein.
29. A method for identifying agonists to the IGS4 neuromedin receptor protein comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8 according to claim 28, wherein said agonists are effective with regard to disorders of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), disorders of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal

muscle and/or of the thyroid, and/or also to lung diseases, immunological diseases and disorders of the genitourinary system.

30. An agonist identified by the method of claim 28 or 29, preferably an agonist being effective with regard to disorders of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), disorders of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal muscle and/or of the thyroid, and/or also to lung diseases, immunological diseases and disorders of the genitourinary system.
31. A method for identifying antagonists to the IGS4 polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8 of claim 17-21 comprising:
  - (a) contacting a cell which produces said IGS4 polypeptide with an agonist; and
  - (b) determining whether the signal generated by said agonist is diminished in the presence of a candidate compound.
32. An antagonist identified by the method of claim 31.
33. A method for identifying antagonists to the IGS4 neuromedin receptor protein comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8, preferably to the mammalian IGS4 neuromedin receptor protein, said protein exhibiting high affinity binding for neuromedin U, preferably for neuromedin U-8, for neuromedin U-23 and/or for neuromedin U-25, comprising:
  - (a) contacting a cell which produces said IGS4 neuromedin receptor protein with an agonist; and
  - (b) determining whether the signal generated by said agonist is diminished in the presence of a candidate compound.
34. A method for identifying antagonists to the IGS4 neuromedin receptor protein comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8 according to claim 33, wherein said antagonists are effective with regard to disorders of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), disorders of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal

muscle and/or of the thyroid, and/or also to lung diseases, immunological diseases and disorders of the genitourinary system.

35. An antagonist identified by the method of claim 33 or 34, preferably an antagonist being effective with regard to disorders of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), disorders of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal muscle and/or of the thyroid, and/or also to lung diseases, immunological diseases and disorders of the genitourinary system.
36. A recombinant host cell produced by a method of claim 16 or a membrane thereof expressing an IGS4 polypeptide.
37. A method of creating a genetically modified non-human animal for IGS4 neuromedin receptor related disorders comprising the steps of:
- (a) ligating the coding portion of a nucleic acid molecule, consisting essentially of a nucleic acid sequence encoding a protein having the amino acid sequence SEQ ID NO: 2, SEQ ID NO: 4, SEQ NO: 6 or SEQ NO: 8 or the amino acid sequence encoded by the DNA insert contained in the deposit no. CBS102221 or the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands, to a regulatory sequence which is capable of driving high level gene expression or expression in a cell type in which the gene is not normally expressed in said animal; or
  - (b) isolation and engineering the coding portion of a nucleic acid molecule, consisting essentially of a nucleic acid sequence encoding a protein having the amino acid sequence SEQ ID NO: 2, SEQ ID NO: 4, SEQ NO: 6 or SEQ NO: 8 or the amino acid sequence encoded by the DNA insert contained in the deposit no. CBS102221 or the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands, and reintroducing said sequence in the genome of said animal in such a way that the endogenous gene alleles, encoding a protein having the amino acid sequence SEQ ID NO: 2, SEQ ID NO: 4, SEQ NO: 6 or SEQ NO: 8 or the amino acid sequence encoded by the DNA insert contained in the deposit no. CBS102221 or the deposit no. CBS102222 at the Centraalbureau voor Schimmelcultures at Baarn the Netherlands, are fully or partially inactivated.

38. A method of determining whether a substance is a potential ligand of IGS4 receptor comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8, comprising:
- (a) contacting cells expressing the receptor of one of the claims 17-21 or one of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8, or contacting a receptor membrane preparation comprising one of said receptors of one of the claims 17-21 or one of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8 with labeled neuromedin U in the presence and in the absence of the substance; and
  - (b) measuring the binding of neuromedin U to said IGS4.
39. A polypeptide according to any of the claims 17-21, further being characterized in that said polypeptide binds neuromedin U, preferably neuromedin U-8, neuromedin U-23 and/or neuromedin U-25, showing at least an affinity of about  $\log EC_{50} = -6$ .
40. A polypeptide according to any of the claims 17-21, further being characterized in that said polypeptide binds neuromedin U, preferably neuromedin U-8, neuromedin U-23 and/or neuromedin U-25, showing at least an affinity of about  $\log EC_{50} = -9$ .

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(81) Designated States (national): AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: **NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR**

(57) Abstract: The present invention relates to novel identified polynucleotides, polypeptides encoded by them and to the use of such polynucleotides and polypeptides, and to their production. More particularly, the polynucleotides and polypeptides of the present invention relate to the G-protein coupled receptor family, referred to as IGS4-family. The invention also relates to inhibiting or activating the action of such polynucleotides and polypeptides, to a vector containing said polynucleotides, a host cell containing such vector and transgenic animals where the IGS4-gene is either overexpressed, misexpressed, underexpressed or suppressed (knock-out animals). The invention further relates to a method for screening compounds capable to act as an agonist or an antagonist of said G-protein coupled receptor family IGS4 and the use of IGS4 polypeptides and polynucleotides and agonists or antagonists to the IGS4 receptor family in the treatment of PNS, psychiatric and CNS disorders, including schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive disorder (OCD), post traumatic stress disorder (PTSD), phobia and panic, major depressive disorder, bipolar disorder, Parkinson's disease, general anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer disease/dementia and other neurodegenerative diseases, severe mental retardation, dyskinesias, Huntington's disease, Tourett's syndrome, tics, tremor, dystonia, spasms, anorexia, bulimia, stroke, addiction/dependency/craving, sleep disorder, epilepsy, migraine; attention deficit/hyperactivity disorder (ADHD); cardiovascular diseases, including heart failure, angina pectoris, arrhythmias, myocardial infarction, cardiac hypertrophy, hypotension, hypertension - e.g. essential hypertension, renal hypertension, or pulmonary hypertension, thrombosis, arteriosclerosis, cerebral vasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney disease - e.g. renal failure; dyslipidemias; obesity; emesis; gastrointestinal disorders, including irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), gastroesophageal reflux disease (GERD), motility disorders and conditions of delayed gastric emptying, such as post operative or diabetic gastroparesis, and diabetes, ulcers - e.g. gastric ulcer; diarrhoea; other diseases including osteoporosis; inflammations; infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; pain; cancers; chemotherapy induced injury; tumor invasion; immune disorders; urinary retention; asthma; allergies; arthritis; benign prostatic hypertrophy; endotoxin shock; sepsis; complication of diabetes mellitus; and gynaecological disorders, among others and diagnostic assays for such conditions. Preferred uses of the invention relate to disorders of the nervous system, including the central nervous system (CNS) and the peripheral nervous system (PNS), disorders of the gastrointestinal system and/or of the cardiovascular system and/or of skeletal muscle and/or of the thyroid, and/or also to lung diseases, immunological diseases and disorders of the genitourinary system. The invention also relates to the identification of the cognate ligand of the IGS4 polypeptides of the invention. High affinity binding to said IGS4 polypeptides is found for the neuropeptides known as neuromedin U.

WO 01/25269 A2

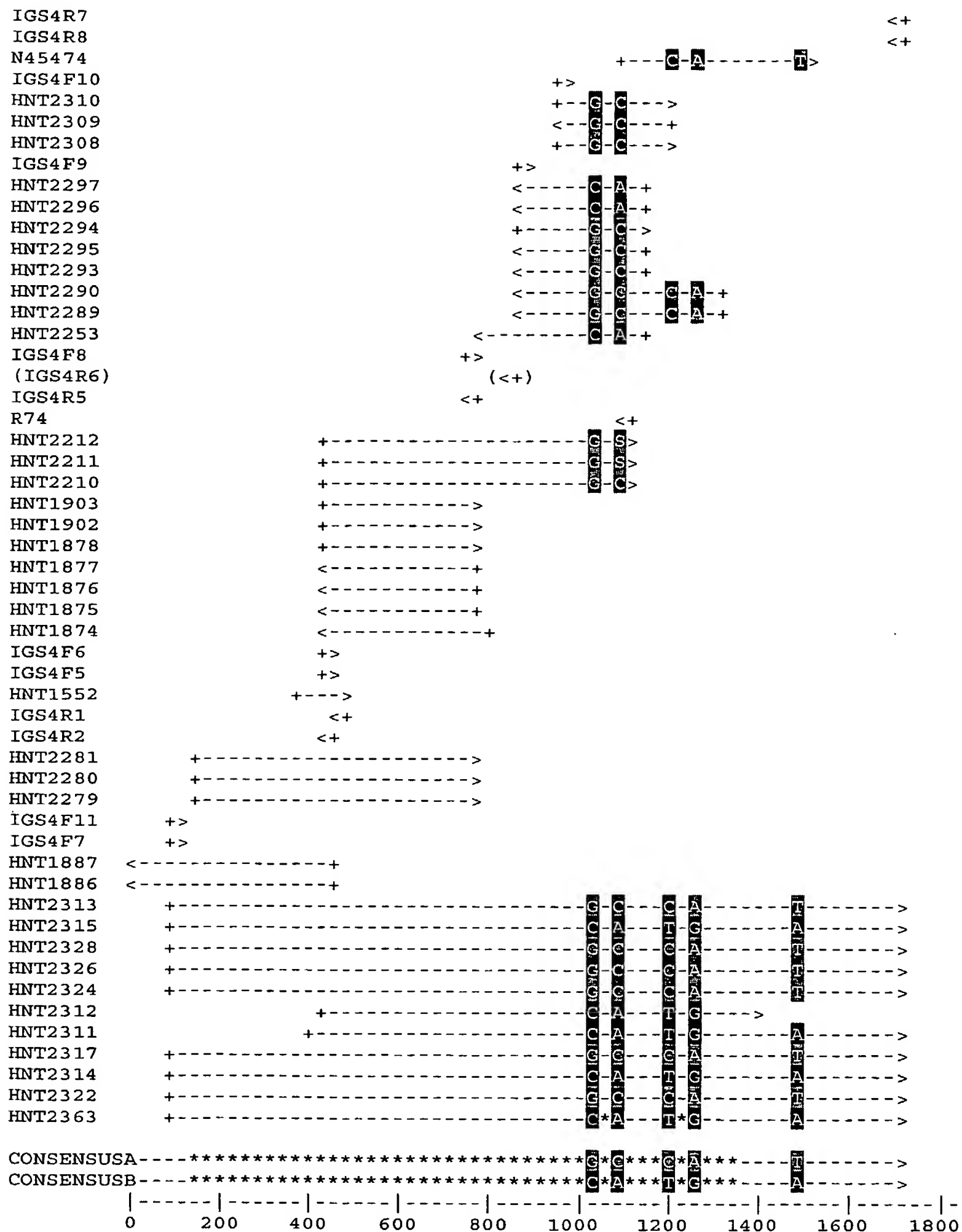
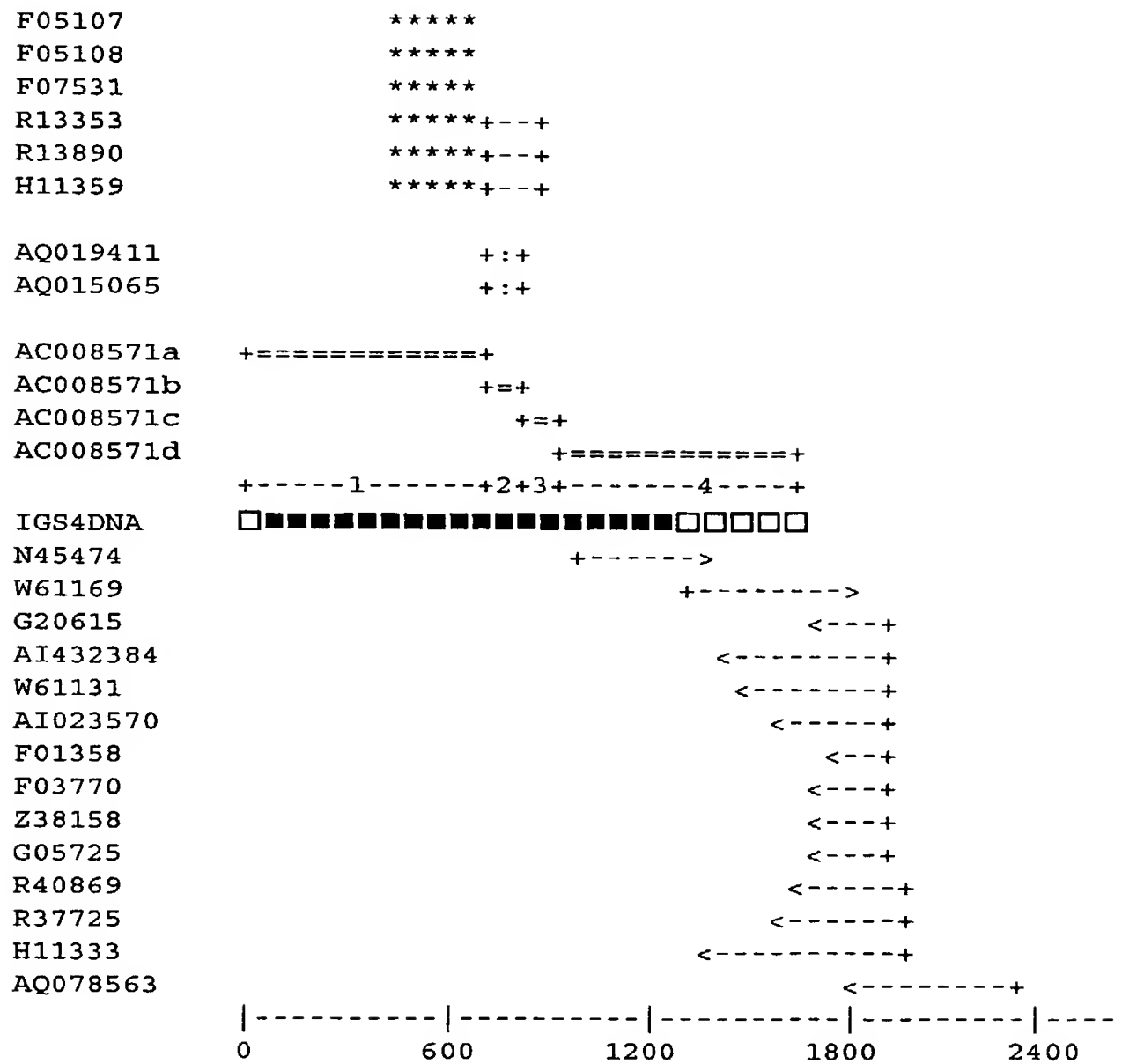


Fig.1





**Fig.2**

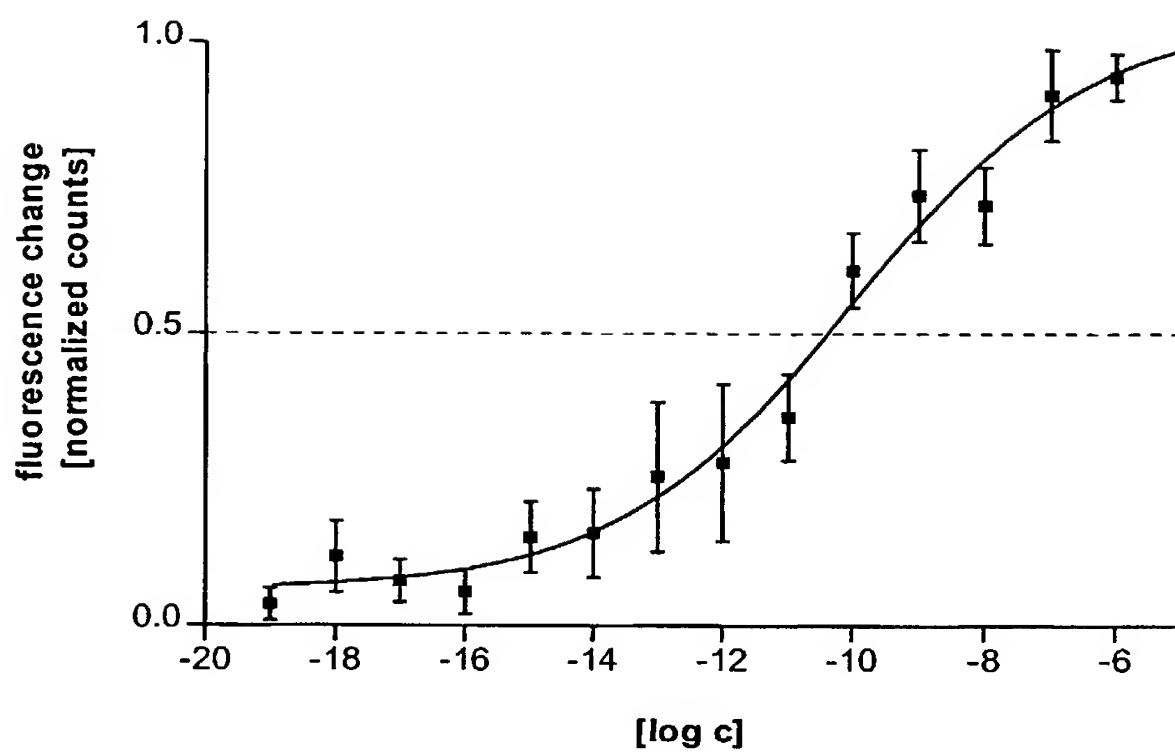


Fig. 3a

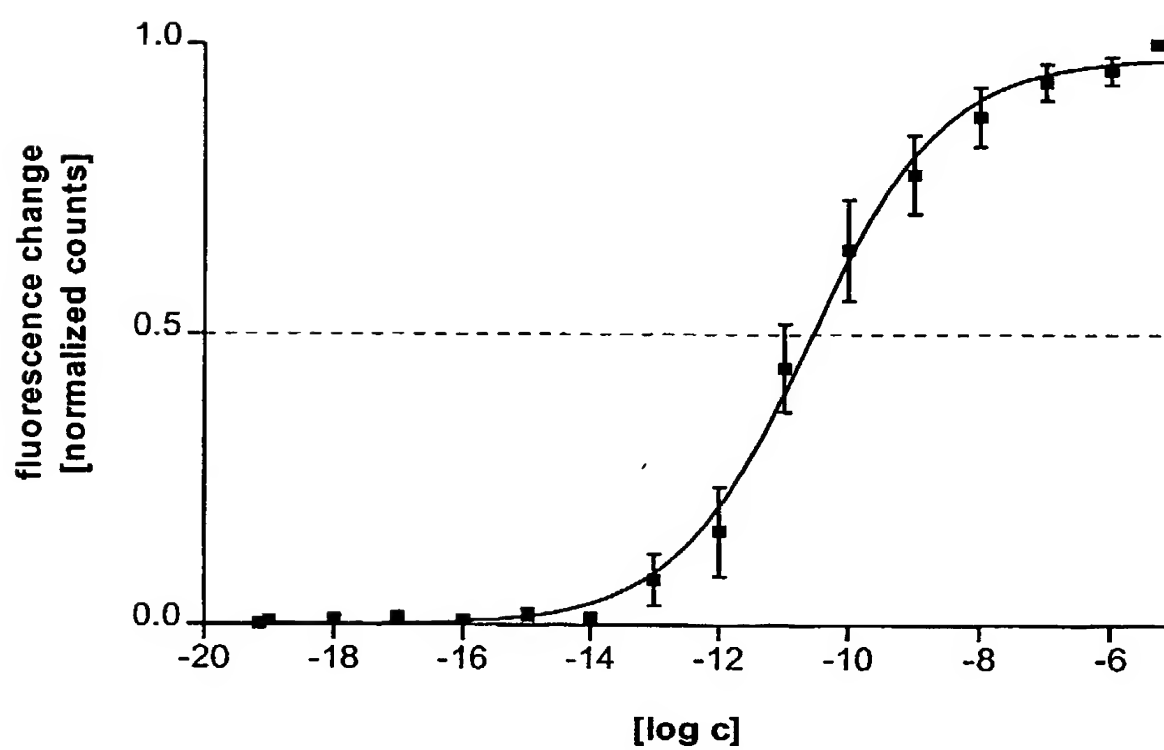


Fig. 3b

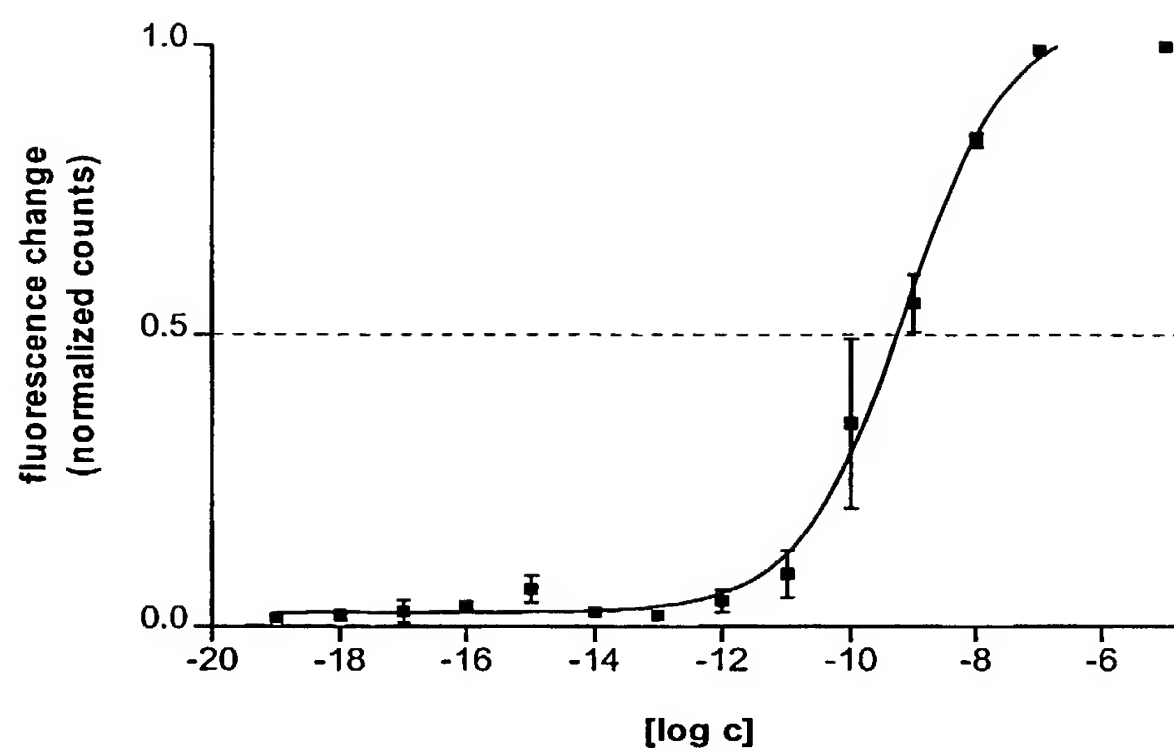
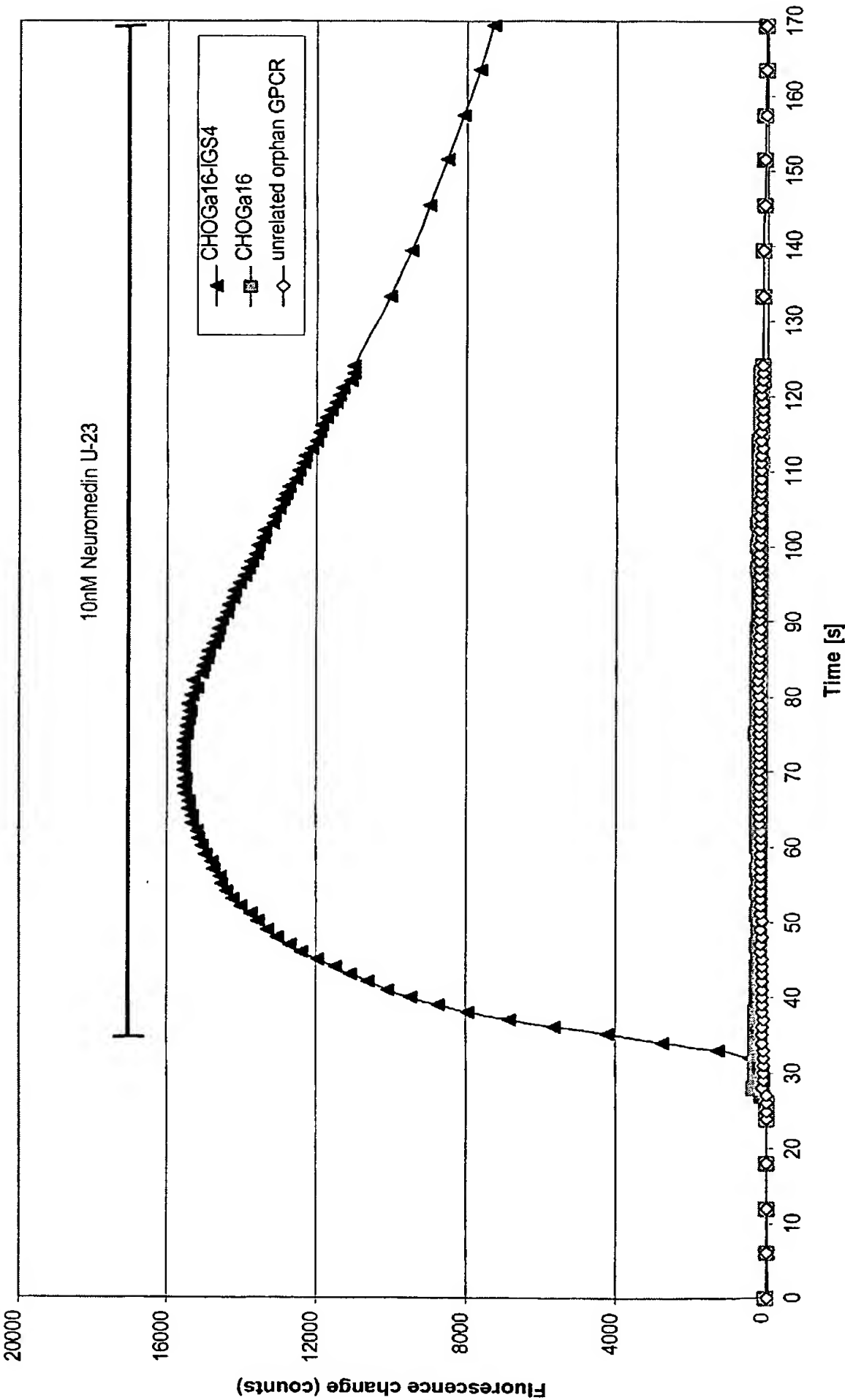


Fig. 3c

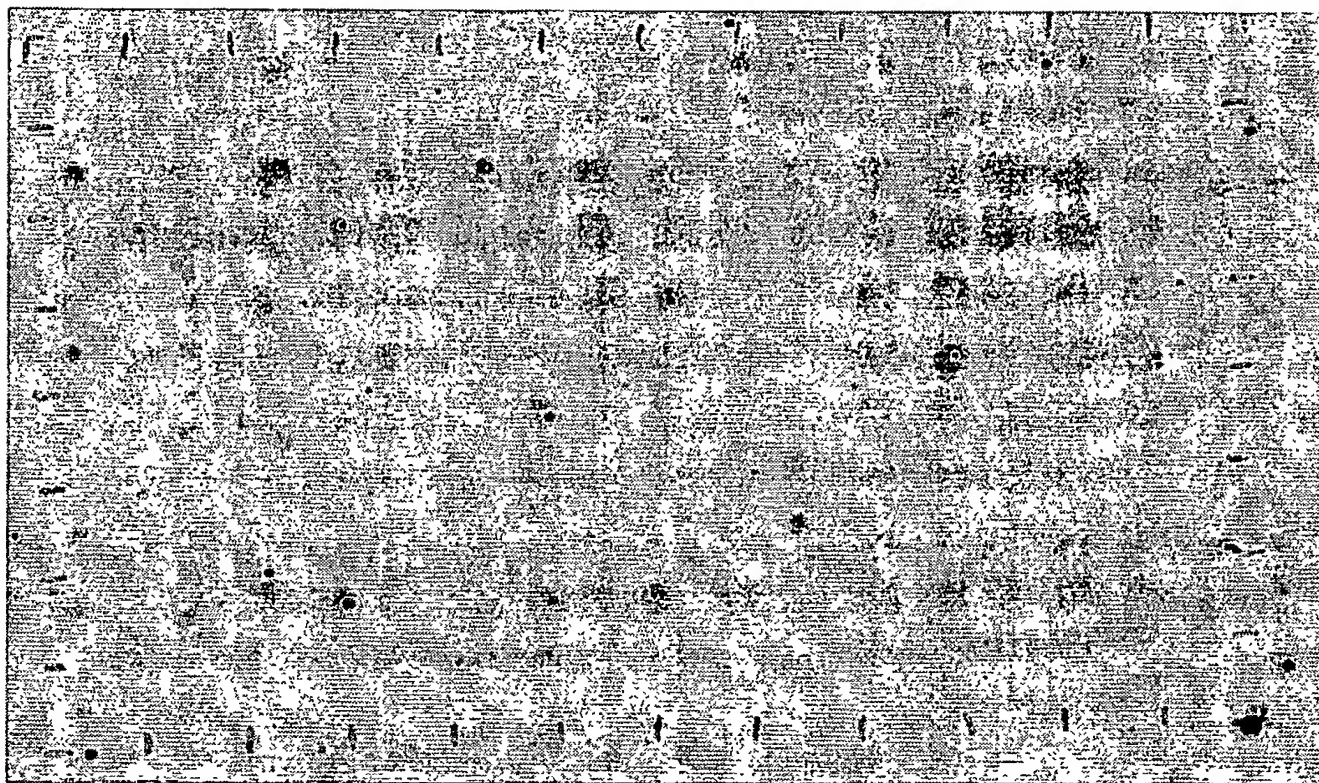
Fig. 4



**Fig. 5**

**1. A1**

**A12**



**2. H1**

**H12**

Human multiple tissue expression array using a human IGS4 probe.

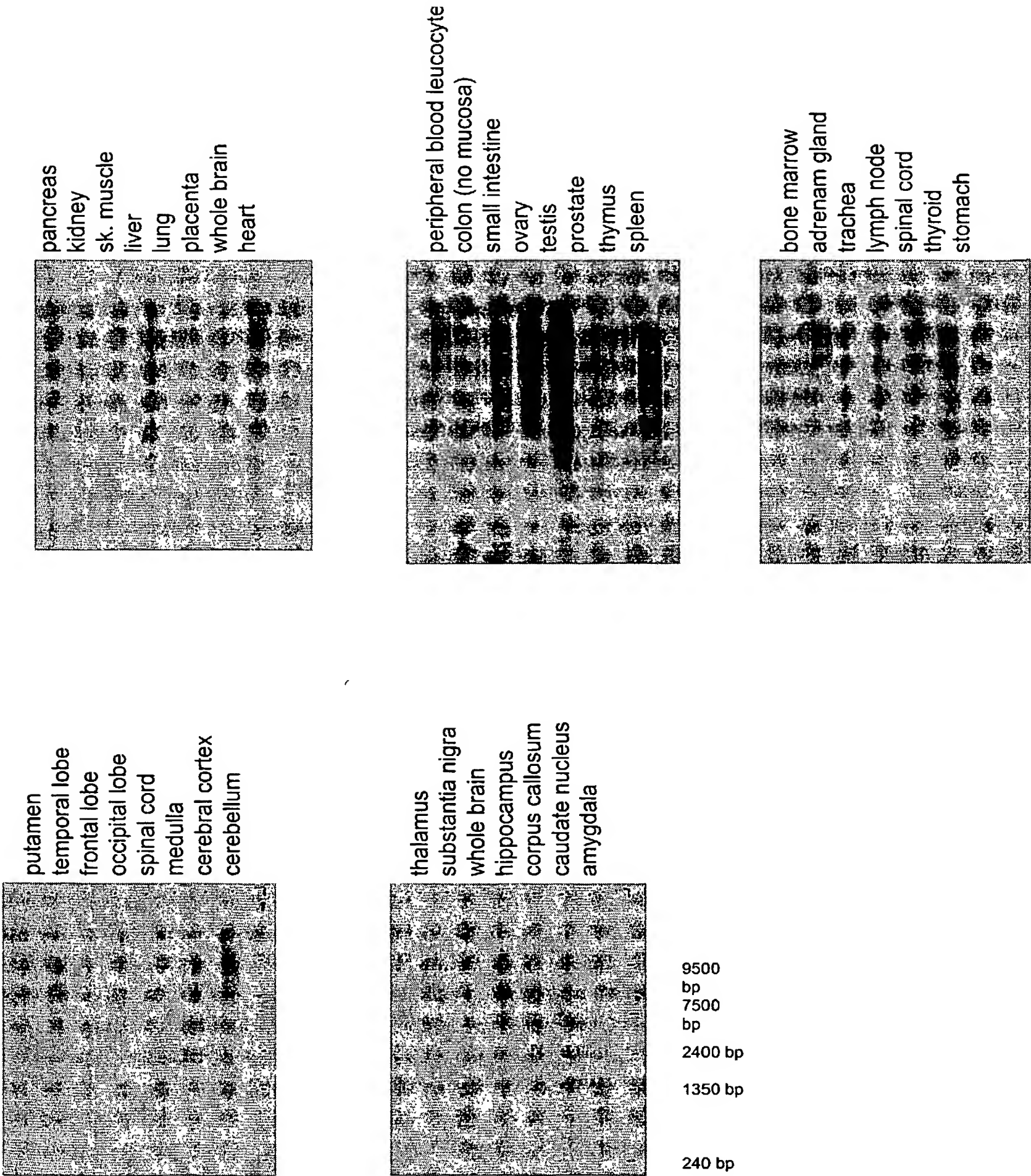


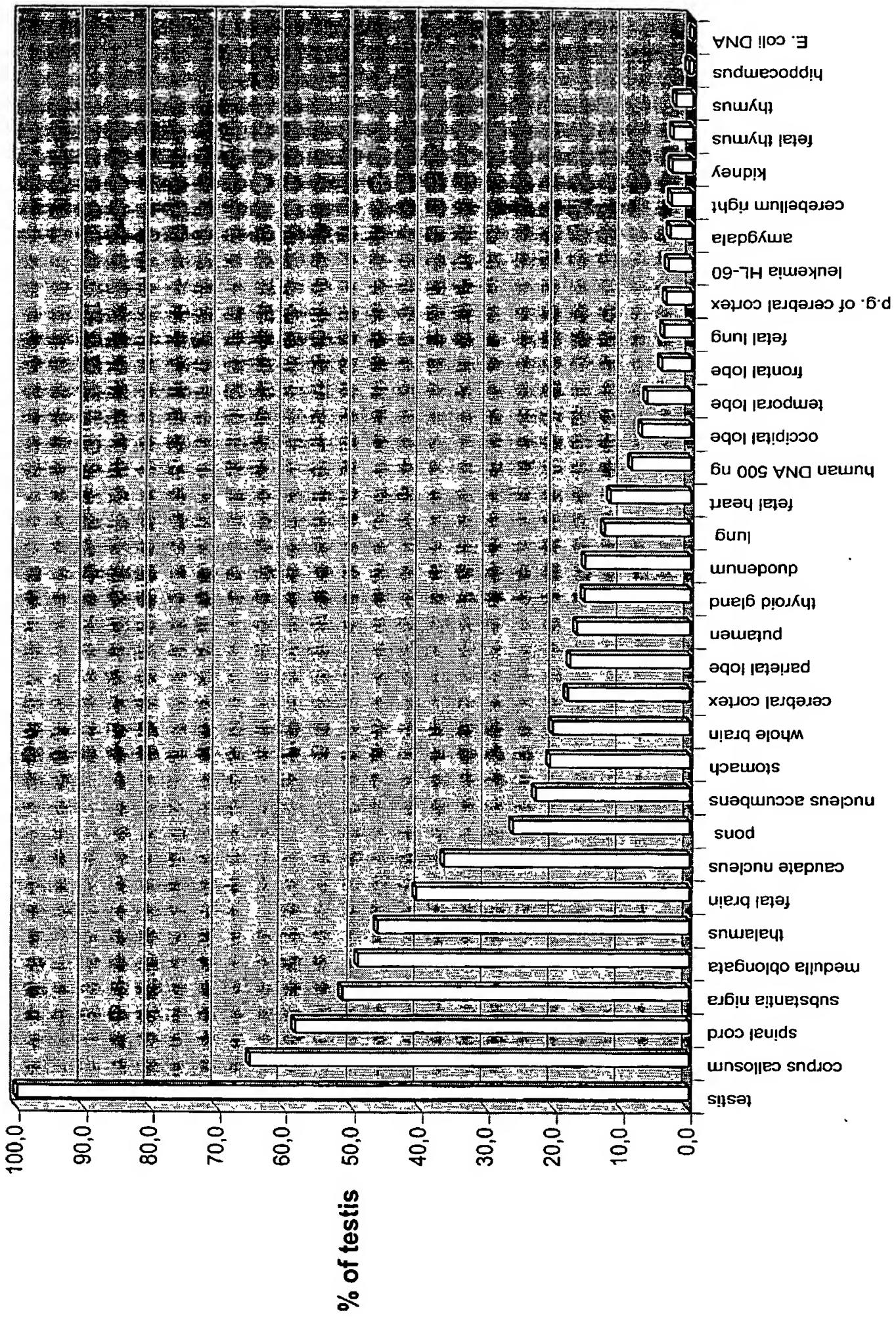
Fig. 6



10/088744

Fig. 7

hu-IGS4 expression analysis (MTE blot)



IGS4 QPCR

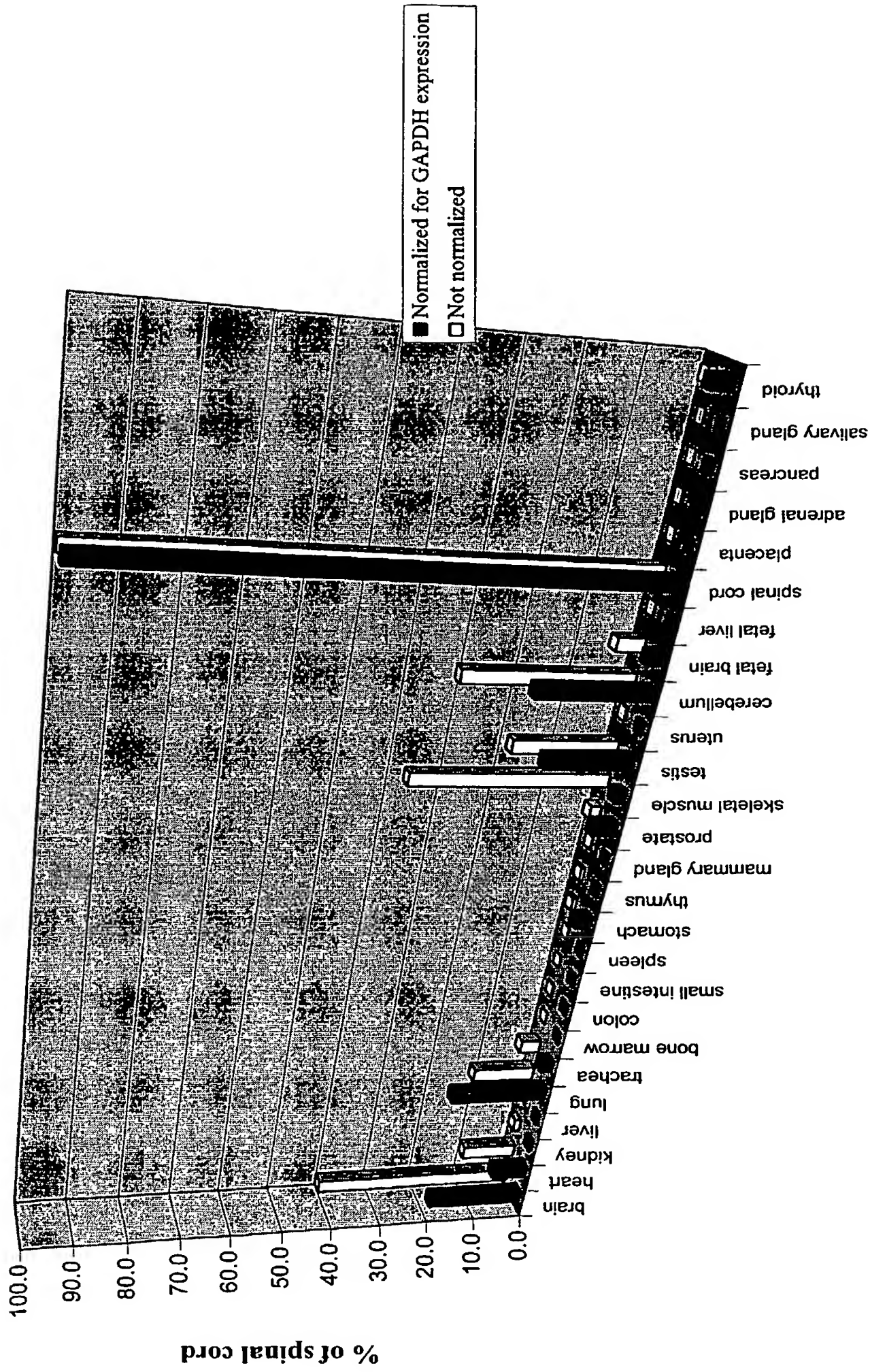


Fig. 8



## DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I/We hereby declare that: my residence, post office address and citizenship are as stated below next to my name; I believe I am the original, first, and sole inventor (if only one name is listed below) or an original, first, and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled: Human G-protein coupled receptor  
the specification of which ☒ is attached and/or ☒ was filed on \_\_\_\_\_ as United States Application Serial No. \_\_\_\_\_ or PCT International Application No. PCT/EP00/09584 and was amended on 14 September 2001

I/We hereby state that I/We have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above. I/We acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR § 1.56.

I/We hereby claim foreign priority benefits under 35 U.S.C. § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate or § 365(a) of any PCT international application(s) designating at least one country other than the United States, listed below and have also identified below, any foreign application(s) for patent or inventor's certificate, or any PCT International application(s) having a filing date before that of the application(s) of which priority is claimed:

Country	Application Number	Date of Filing	Priority Claimed Under 35 U.S.C. 119
EP (NL designated)	99203140.1	24 September 1999	<input checked="" type="checkbox"/> YES <input type="checkbox"/> NO
NL	1013140	24 September 1999	<input checked="" type="checkbox"/> YES <input type="checkbox"/> NO
EP (NL designated)	00202683.9	28 July 2000	<input checked="" type="checkbox"/> YES <input type="checkbox"/> NO

I/We hereby claim the benefit under 35 U.S.C. § 119(e) of any United States provisional application(s) listed below:

Application Number	Date of Filing
66/222,047	31 July 2000

Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P. • Washington, D.C.

Attorney Docket No.: SPW99.06 US  
Declaration/Power of Attorney  
Worldwide Rights

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As a below named inventor, I/We hereby declare that: my residence, post office address and citizenship are as stated below next to my name; I believe I am the original, first, and sole inventor (if only one name is listed below) or an original, first, and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled: Human G-protein coupled receptor the specification of which ☒ is attached and/or ☒ was filed on \_\_\_\_\_ as United States Application Serial No. \_\_\_\_\_ or PCT International Application No. PCT/EP00/09584 and was amended on 14 September 2001

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Application Number	Date of Filing
66/222,047	31 July 2000

I/We hereby claim the benefit under 35 U.S.C. § 120 of any United States application(s) or § 365(c) of any PCT International application(s) designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application(s) in the manner provided by the first paragraph of 35 U.S.C. § 112, I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR § 1.56 which became available between the filing date of the prior application(s) and the national or PCT International filing date of this application:

Application Number	Date of Filing	Status (Patented, Pending, Abandoned)

I/We hereby appoint the following attorney and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith. **FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, L.L.P.**, Douglas B. Henderson, Reg. No. 20,291; Ford F. Farabow, Jr., Reg. No. 20,630; Arthur S. Garrett, Reg. No. 20,338; Donald R. Dunner, Reg. No. 19,073; Brian G. Brunsvold, Reg. No. 22,593; Tipton D. Jennings, IV, Reg. No. 20,645; Jerry D. Voight, Reg. No. 23,020; Laurence R. Heffer, Reg. No. 20,827; Kenneth E. Payne, Reg. No. 23,098; Herbert H. Mintz, Reg. No. 26,691; C. Larry O'Rourke, Reg. No. 26,014; Albert J. Santorelli, Reg. No. 22,610; Michael C. Elmer, Reg. No. 25,857; Richard H. Smith, Reg. No. 20,609; Stephen L. Peterson, Reg. No. 26,325; John M. Romary, Reg. No. 26,331; Bruce C. Zotter, Reg. No. 27,680; Dennis P. O'Reilly, Reg. No. 27,932; Allen M. Sokal, Reg. No. 26,695; Robert D. Bajefsky, Reg. No. 25,387; Richard L. Stroup, Reg. No. 28,478; David W. Hill, Reg. No. 28,220; Thomas L. Irving, Reg. No. 28,619; Charles E. Lipsey, Reg. No. 28,165; Thomas W. Winland, Reg. No. 27,605; Basil J. Lewris, Reg. No. 28,818; Martin I. Fuchs, Reg. No. 28,508; E. Robert Yoches, Reg. No. 30,120; Barry W. Graham, Reg. No. 29,924; Susan Haberman Griffen, Reg. No. 30,907; Richard B. Racine, Reg. No. 30,415; Thomas H. Jenkins, Reg. No. 30,857; Robert E. Converse, Jr., Reg. No. 27,432; Clair X. Mullen, Jr., Reg. No. 20,348; Christopher P. Foley, Reg. No. 31,354; John C. Paul, Reg. No. 30,413; Roger D. Taylor, Reg. No. 28,992; David M. Kelly, Reg. No. 30,953; Kenneth J. Meyers, Reg. No. 25,146; Carol P. Einaudi, Reg. No. 32,220; Walter Y. Boyd, Jr., Reg. No. 31,738; Steven M. Anzalone, Reg. No. 32,095; Jean B. Fordis, Reg. No. 32,984; Barbara C. McCurdy, Reg. No. 32,120; James K. Hammond, Reg. No. 31,964; Richard V. Burgujian, Reg. No. 31,744; J. Michael Jakes, Reg. No. 32,824; Dirk D. Thomas, Reg. No. 32,600; Thomas W. Banks, Reg. No. 32,719; Christopher P. Isaac, Reg. No. 32,616; Bryan C. Diner, Reg. No. 32,409; M. Paul Barker, Reg. No. 32,013; Andrew Chanhon Sonu, Reg. No. 33,457; David S. Forman, Reg. No. 33,694; Vincent P. Kovalick, Reg. No. 32,867; James W. Edmondson, Reg. No. 33,871; Michael R. McGurk, Reg. No. 32,045; Joann M. Neth, Reg. No. 36,363; Gerson S. Panitch, Reg. No. 33,751; Cheri M. Taylor, Reg. No. 33,216; Charles E. Van Horn, Reg. No. 40,266; Linda A. Wadler, Reg. No. 33,218; Jeffrey A. Berkowitz, Reg. No. 36,743; Michael R. Kelly, Reg. No. 33,921; and James B. Monroe, Reg. No. 33,971; and \_\_\_\_\_.

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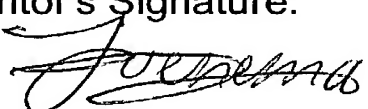
IN TESTIMONY WHEREOF, I/We have hereunto set our hands.

1-00 Full Name of First Inventor: <u>Willy Deleersnijder</u>	Inventor's Signature: <u>Willy Deleersnijder</u>	Date: <u>January 24, 2002</u>
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Post Office Address: C.J. van Houtenlaan 36, 1381 CP Weesp, The Netherlands		
2-00 Full Name of Second Inventor: <u>Guy Nys</u>	Inventor's Signature: <u>Guy Nys</u>	Date: <u>January 24, 2002</u>
Residence: <u>Weesp</u> , The Netherlands <u>NLX</u>		Citizenship: Belgian
Post Office Address: C.J. van Houtenlaan 36, 1381 CP Weesp, The Netherlands		

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I/We hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

IN TESTIMONY WHEREOF, I/We have hereunto set our hands.

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Post Office Address: C.J. van Houtenlaan 36, 1381 CP Weesp, The Netherlands		

1/28

## SEQUENCE LISTING

&lt;110&gt; SOLVAY PHARMACEUTICALS B.V.

&lt;120&gt; Novel human G-protein coupled Receptor

&lt;130&gt; SPW99.06/HA 00.19

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2/28

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3/28

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&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val			
35	40	45	
Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val			
50	55	60	
Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr			
65	70	75	80

4/28

Asn	Tyr	Tyr	Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu
				85					90					95	
Leu	Gly	Met	Pro	Leu	Glu	Val	Tyr	Glu	Met	Trp	Arg	Asn	Tyr	Pro	Phe
			100					105					110		
Leu	Phe	Gly	Pro	Val	Gly	Cys	Tyr	Phe	Lys	Thr	Ala	Leu	Phe	Glu	Thr
		115					120						125		
Val	Cys	Phe	Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg
	130					135					140				
Tyr	Val	Ala	Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg
145					150					155					160
Arg	Arg	Ala	Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu
				165					170					175	
Phe	Ser	Leu	Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe
			180					185					190		
Pro	Asn	Gly	Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys
		195					200					205			
Pro	Met	Trp	Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe
	210					215					220				
Tyr	Leu	Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala
225					230					235					240
Leu	Arg	Leu	Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala
				245					250					255	
Asn	Ile	Gln	Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Phe	Val
			260					265					270		
Leu	Val	Leu	Val	Phe	Ala	Ile	Cys	Trp	Ala	Pro	Phe	His	Ile	Asp	Arg
		275					280					285			
Leu	Phe	Phe	Ser	Phe	Val	Glu	Glu	Trp	Ser	Glu	Ser	Leu	Ala	Ala	Val
	290					295					300				
Phe	Asn	Leu	Val	His	Val	Val	Ser	Gly	Val	Phe	Phe	Tyr	Leu	Ser	Ser
305					310					315					320
Ala	Val	Asn	Pro	Ile	Ile	Tyr	Asn	Leu	Leu	Ser	Arg	Arg	Phe	Gln	Ala
				325					330					335	
Ala	Phe	Gln	Asn	Val	Ile	Ser	Ser	Phe	His	Lys	Gln	Trp	His	Ser	Gln
			340					345					350		
His	Asp	Pro	Gln	Leu	Pro	Pro	Ala	Gln	Arg	Asn	Ile	Phe	Leu	Thr	Glu
		355					360					365			
Cys	His	Phe	Val	Glu	Leu	Thr	Glu	Asp	Ile	Gly	Pro	Gln	Phe	Pro	Cys
	370					375					380				

5/28

Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu  
 385 390 395 400

Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr  
 405 410 415

&lt;210&gt; 3

&lt;211&gt; 1658

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (64)..(1299)

&lt;223&gt; IGS4A short version

&lt;400&gt; 3

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 Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu  
 1 5 10 15

gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156  
 Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala  
 20 25 30

ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct gtg 204  
 Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val  
 35 40 45

gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg gtg 252  
 Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val  
 50 55 60

tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac tac 300  
 Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr  
 65 70 75

tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt gga 348  
 Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly  
 80 85 90 95

atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg ttc 396  
 Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe  
 100 105 110

ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg tgc 444  
 Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys  
 115 120 125

ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac gtg 492  
 Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val

6/28

130	135	140	
gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc cgg Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg 145 150 155			540
gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc tcc Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser 160 165 170 175			588
ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc aat Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn 180 185 190			636
ggg tcc ctg gtc cca ggt tcc gcc acc tgt acg gtc atc aag ccc atg Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met 195 200 205			684
tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac ctc Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu 210 215 220			732
ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc aga Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg 225 230 235			780
cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat att Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile 240 245 250 255			828
caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg gtc Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu Val 260 265 270			876
tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc ttc Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu Phe 275 280 285			924
ttc agc ttt gtg gag gag tgg agt gaa tcc ctg gct gct gtg ttc aac Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val Phe Asn 290 295 300			972
ctc gtc cat gtg gtg tca ggt gtc ttc ttc tac ctg agc tca gct gtc Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser Ala Val 305 310 315			1020
aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca ttc Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala Phe 320 325 330 335			1068
cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat gac Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His Asp 340 345 350			1116
cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc cac Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys His 1164			

7/28

355 360 365  
 ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cca tgt cag tca 1212  
 Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys Gln Ser  
 370 375 380  
 tcc atg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag atg 1260  
 Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln Met  
 385 390 395  
 tca aga aca aac tat caa agc ttc cac ttt aac aaa acc tgaattcttt 1309  
 Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr  
 400 405 410  
 cagagctgac tctcctctat gcctcaaaac ttcagagagg aacatcccat aatgtatgcc 1369  
 ttctcatatg atattagaga ggtagaatgg ctcttacaac tcatgtaccc attgctagtt 1429  
 tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac ccaagactgc 1489  
 ctgattttta gttatctttc cactatccta actgcctcat gccccttcac tagttcatgc 1549  
 caagaacgtg actggaaagg catggcacct ataccttgat taattttccat taatggaaat 1609  
 ggttcgtcct gagtcatcta cgttccgagt caggctgtca ctcctacta 1658  
  
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 <212> PRT  
 <213> Homo sapiens  
  
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 20 25 30  
 Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val Val  
 35 40 45  
 Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val Cys  
 50 55 60  
 Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr Tyr  
 65 70 75 80  
 Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly Met  
 85 90 95  
 Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe Gly  
 100 105 110  
 Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys Phe  
 115 120 125

8/28

Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg	Tyr	Val	Ala	130	135	140
Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg	Arg	Ala	145	150	155
Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu	Phe	Ser	Leu	165	170	175
Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	Asn	Gly	180	185	190
Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	Pro	Met	Trp	195	200	205
Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	Tyr	Leu	Leu	210	215	220
Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	Arg	Leu	225	230	235
Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala	Asn	Ile	Gln	245	250	255
Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Phe	Val	Leu	Val	Leu	260	265	270
Val	Phe	Ala	Ile	Cys	Trp	Ala	Pro	Phe	His	Ile	Asp	Arg	Leu	Phe	Phe	275	280	285
Ser	Phe	Val	Glu	Glu	Trp	Ser	Glu	Ser	Leu	Ala	Ala	Val	Phe	Asn	Leu	290	295	300
Val	His	Val	Val	Ser	Gly	Val	Phe	Phe	Tyr	Leu	Ser	Ser	Ala	Val	Asn	305	310	315
Pro	Ile	Ile	Tyr	Asn	Leu	Leu	Ser	Arg	Arg	Phe	Gln	Ala	Ala	Phe	Gln	325	330	335
Asn	Val	Ile	Ser	Ser	Phe	His	Lys	Gln	Trp	His	Ser	Gln	His	Asp	Pro	340	345	350
Gln	Leu	Pro	Pro	Ala	Gln	Arg	Asn	Ile	Phe	Leu	Thr	Glu	Cys	His	Phe	355	360	365
Val	Glu	Leu	Thr	Glu	Asp	Ile	Gly	Pro	Gln	Phe	Pro	Cys	Gln	Ser	Ser	370	375	380
Met	His	Asn	Ser	His	Leu	Pro	Thr	Ala	Leu	Ser	Ser	Glu	Gln	Met	Ser	385	390	395
Arg	Thr	Asn	Tyr	Gln	Ser	Phe	His	Phe	Asn	Lys	Thr					405	410	

9/28

<210> 5  
 <211> 1658  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (55)..(1299)  
 <223> IGS4B long version

<400> 5

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ggctcagctt gaaacagagc ctcgtagcagg gggagggtca ggccttggat ttta atg  57
                                                    Met
                                                    1

tca ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa  105
Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys
           5                      10                      15

cta gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg  153
Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu
           20                      25                      30

gcc ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct  201
Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser
           35                      40                      45

gtg gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg  249
Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu
           50                      55                      60                      65

gtg tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac  297
Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn
           70                      75                      80

tac tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt  345
Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu
           85                      90                      95

gga atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg  393
Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu
           100                      105                      110

ttc ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg  441
Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val
           115                      120                      125

tgc ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac  489
Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr
           130                      135                      140                      145

gtg gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc  537
Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg
           150                      155                      160

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10/28

cgg gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc	585
Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe	
165 170 175	
tcc ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc	633
Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro	
180 185 190	
aat ggg tcc ctg gtc cca ggt tcg gcc acc tgt acg gtc atc aag ccc	681
Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro	
195 200 205	
atg tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac	729
Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr	
210 215 220 225	
ctc ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc	777
Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu	
230 235 240	
aga cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat	825
Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn	
245 250 255	
att caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg	873
Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu	
260 265 270	
gtc tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc	921
Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu	
275 280 285	
ttc ttc agc ttt gtg gag gag tgg act gaa tcc ctg gct gct gtg ttc	969
Phe Phe Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val Phe	
290 295 300 305	
aac ctc gtc cat gtg gtg tca ggt gtc tta ttc tac ctg agc tca gct	1017
Asn Leu Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser Ala	
310 315 320	
gtc aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca	1065
Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala	
325 330 335	
ttc cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat	1113
Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His	
340 345 350	
gac cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc	1161
Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys	
355 360 365	
cac ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cta tgt cag	1209
His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys Gln	
370 375 380 385	

11/28

tca tcc gtg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag 1257  
 Ser Ser Val His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln  
                     390                    395                    400

atg tca aga aca aac tat caa agc ttc cac ttt aac aaa acc 1299  
 Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr  
                     405                    410                    415

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 aatgtatgcc ttctcatatg aaattagaga ggtagaatgg ctcttacaac tcatgtaccc 1419  
 attgctagtt tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac 1479  
 ccaagactgc ctgattttta gttatctttc cactatccta actgcctcat gccccttcac 1539  
 tagttcatgc caagaacgtg actggaaagg catggcacct ataccttgat taatttccat 1599  
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&lt;210&gt; 6

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

Met Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln  
   1                    5                    10                    15

Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr  
                     20                    25                    30

Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val  
                     35                    40                    45

Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val  
                     50                    55                    60

Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr  
   65                    70                    75                    80

Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu  
                     85                    90                    95

Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe  
                     100                    105                    110

Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr  
                     115                    120                    125

Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg  
                     130                    135                    140

Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg  
   145                    150                    155                    160

[illegible][illegible][illegible]

13/28

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (64)..(1299)

&lt;223&gt; IGS4B short version

&lt;400&gt; 7

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Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu
1 5 10 15

gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156
Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala
20 25 30

ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct gtg 204
Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val
35 40 45

gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg gtg 252
Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val
50 55 60

tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac tac 300
Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr
65 70 75

tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt gga 348
Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly
80 85 90 95

atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg ttc 396
Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe
100 105 110

ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg tgc 444
Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys
115 120 125

ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac gtg 492
Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val
130 135 140

gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc cgg 540
Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg
145 150 155

gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc tcc 588
Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser
160 165 170 175

ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc aat 636
Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn
180 185 190

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WO 01/25269

PCT/EP00/09584

14/28

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Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met	
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tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac ctc	732
Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu	
210 215 220	
ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc aga	780
Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg	
225 230 235	
cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat att	828
Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile	
240 245 250 255	
caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg gtc	876
Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu Val	
260 265 270	
tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc ttc	924
Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu Phe	
275 280 285	
ttc agc ttt gtg gag gag tgg act gaa tcc ctg gct gct gtg ttc aac	972
Phe Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val Phe Asn	
290 295 300	
ctc gtc cat gtg gtg tca ggt gtc tta ttc tac ctg agc tca gct gtc	1020
Leu Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser Ala Val	
305 310 315	
aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca ttc	1068
Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala Phe	
320 325 330 335	
cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat gac	1116
Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His Asp	
340 345 350	
cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc cac	1164
Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys His	
355 360 365	
ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cta tgt cag tca	1212
Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys Gln Ser	
370 375 380	
tcc gtg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag atg	1260
Ser Val His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln Met	
385 390 395	
tca aga aca aac tat caa agc ttc cac ttt aac aaa acc tgaattcttt	1309
Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr	
400 405 410	

15/28

cagagctgac tctcctctat gcctcaaaac ttcagagagg aacatcccat aatgtatgcc 1369  
 ttctcatatg aaattagaga ggtagaatgg ctcttacaac tcatgtaccc attgctagtt 1429  
 tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac ccaagactgc 1489  
 ctgattttta gttatctttc cactatccta actgcctcat gccccttcac tagttcatgc 1549  
 caagaacgtg actggaaagg catggcacct ataccttgat taatttccat taatggaaat 1609  
 gggtcgtcct gagtcatcta cgttccgagt caggctgtca ctctacta 1658

&lt;210&gt; 8

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

Met	Glu	Lys	Leu	Gln	Asn	Ala	Ser	Trp	Ile	Tyr	Gln	Gln	Lys	Leu	Glu
1				5					10					15	
Asp	Pro	Phe	Gln	Lys	His	Leu	Asn	Ser	Thr	Glu	Glu	Tyr	Leu	Ala	Phe
			20					25					30		
Leu	Cys	Gly	Pro	Arg	Arg	Ser	His	Phe	Phe	Leu	Pro	Val	Ser	Val	Val
		35					40					45			
Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val	Leu	Val	Cys
	50					55					60				
Leu	Val	Ile	Leu	Gln	His	Gln	Ala	Met	Lys	Thr	Pro	Thr	Asn	Tyr	Tyr
65					70					75					80
Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu	Leu	Gly	Met
				85					90					95	
Pro	Leu	Glu	Val	Tyr	Glu	Met	Trp	Arg	Asn	Tyr	Pro	Phe	Leu	Phe	Gly
			100					105					110		
Pro	Val	Gly	Cys	Tyr	Phe	Lys	Thr	Ala	Leu	Phe	Glu	Thr	Val	Cys	Phe
		115					120					125			
Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg	Tyr	Val	Ala
		130				135					140				
Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg	Arg	Ala
145					150					155					160
Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu	Phe	Ser	Leu
				165					170					175	
Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	Asn	Gly
			180					185					190		
Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	Pro	Met	Trp

16/28

195					200					205						
Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	Tyr	Leu	Leu	
210					215					220						
Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	Arg	Leu	
225					230					235					240	
Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala	Asn	Ile	Gln	
245					250					255						
Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Phe	Val	Leu	Val	Leu	
260					265					270						
Val	Phe	Ala	Ile	Cys	Trp	Ala	Pro	Phe	His	Ile	Asp	Arg	Leu	Phe	Phe	
275					280					285						
Ser	Phe	Val	Glu	Glu	Trp	Thr	Glu	Ser	Leu	Ala	Ala	Val	Phe	Asn	Leu	
290					295					300						
Val	His	Val	Val	Ser	Gly	Val	Leu	Phe	Tyr	Leu	Ser	Ser	Ala	Val	Asn	
305					310					315					320	
Pro	Ile	Ile	Tyr	Asn	Leu	Leu	Ser	Arg	Arg	Phe	Gln	Ala	Ala	Phe	Gln	
325					330					335						
Asn	Val	Ile	Ser	Ser	Phe	His	Lys	Gln	Trp	His	Ser	Gln	His	Asp	Pro	
340					345					350						
Gln	Leu	Pro	Pro	Ala	Gln	Arg	Asn	Ile	Phe	Leu	Thr	Glu	Cys	His	Phe	
355					360					365						
Val	Glu	Leu	Thr	Glu	Asp	Ile	Gly	Pro	Gln	Phe	Leu	Cys	Gln	Ser	Ser	
370					375					380						
Val	His	Asn	Ser	His	Leu	Pro	Thr	Ala	Leu	Ser	Ser	Glu	Gln	Met	Ser	
385					390					395					400	
Arg	Thr	Asn	Tyr	Gln	Ser	Phe	His	Phe	Asn	Lys	Thr					
405					410											

&lt;210&gt; 9

&lt;211&gt; 1594

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (55)..(942)

&lt;223&gt; IGS4A truncated DNA long version

&lt;400&gt; 9

ggctcagctt gaaacagagc ctcgtaccag gggaggctca ggccttggat ttta atg 57  
Met

17/28

1

tca ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa	105
Ser Gly Met. Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys	
5 10 15	
cta gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg	153
Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu	
20 25 30	
gcc ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct	201
Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser	
35 40 45	
gtg gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg	249
Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu	
50 55 60 65	
gtg tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac	297
Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn	
70 75 80	
tac tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt	345
Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu	
85 90 95	
gga atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg	393
Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu	
100 105 110	
ttc ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg	441
Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val	
115 120 125	
tgc ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac	489
Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr	
130 135 140 145	
gtg gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc	537
Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg	
150 155 160	
cgg gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc	585
Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe	
165 170 175	
tcc ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc	633
Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro	
180 185 190	
aat ggg tcc ctg gtc cca ggt tcg gcc acc tgt acg gtc atc aag ccc	681
Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro	
195 200 205	
atg tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac	729
Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr	



WO 01/25269

PCT/EP00/09584

18/28

210	215	220	225	
ctc ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc				777
Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu				
	230	235	240	
aga cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat				825
Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn				
	245	250	255	
att caa aga ccc tgc aga aaa tca gtc aac aag atg ctg tct ttg tgg				873
Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu Trp				
	260	265	270	
agg agt gga gtg aat ccc tgg ctg ctg tgt tca acc tcg tcc atg tgg				921
Arg Ser Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met Trp				
	275	280	285	
tgt cag gtg tct tct tct acc tgagctcagc tgtcaacccc attatctata				972
Cys Gln Val Ser Ser Ser Thr				
	290	295		
acctactgtc tcgccgcttc caggcagcat tccagaatgt gatctcttct ttccacaaac 1032				
agtggcactc ccagcatgac ccacagttgc cacctgccc a gcggaacatc ttcctgacag 1092				
aatgccactt tgtggagctg accgaagata taggtcccca attcccatgt cagtcatcca 1152				
tgcacaactc tcacctccca acagccctct ctagtgaaca gatgtcaaga acaaactatc 1212				
aaagcttcca ctttaacaaa acctgaattc tttcagagct gactctcctc tatgcctcaa 1272				
aacttcagag aggaacatcc cataatgtat gccttctcat atgatattag agaggtagaa 1332				
tggctcttac aactcatgta cccattgcta gttttttttt ttttaataaac gtgaaaactg 1392				
agagttagat ctggtttcaa aaccaagac tgccctgattt ttagttatct ttccactatc 1452				
ctaactgcct catgcccctt cactagttca tgccaagaac gtgactggaa aggcattggca 1512				
cctatacctt gattaatttc cattaatgga aatggttcgt cctgagtcac ctacgttccg 1572				
agtcaggctg tcactcctac ta 1594				

<210> 10

<211> 296

<212> PRT

<213> Homo sapiens

<400> 10

Met	Ser	Gly	Met	Glu	Lys	Leu	Gln	Asn	Ala	Ser	Trp	Ile	Tyr	Gln	Gln
1				5					10					15	

Lys	Leu	Glu	Asp	Pro	Phe	Gln	Lys	His	Leu	Asn	Ser	Thr	Glu	Glu	Tyr
			20					25					30		

19/28

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Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val
    35                                40                                45

Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val
    50                                55                                60

Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr
    65                                70                                75                                80

Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu
    85                                90                                95

Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe
    100                                105                                110

Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr
    115                                120                                125

Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg
    130                                135                                140

Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg
    145                                150                                155                                160

Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu
    165                                170                                175

Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe
    180                                185                                190

Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys
    195                                200                                205

Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe
    210                                215                                220

Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala
    225                                230                                235                                240

Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala
    245                                250                                255

Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu
    260                                265                                270

Trp Arg Ser Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met
    275                                280                                285

Trp Cys Gln Val Ser Ser Ser Thr
    290                                295

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&lt;210&gt; 11

&lt;211&gt; 1594

20/28

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (64)..(942)

&lt;223&gt; IGS4A truncated DNA short version

&lt;400&gt; 11

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ggctcagctt gaaacagagc ctcgtaccag gggagggtca ggccttggat tttaatgtca 60

ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa cta 108
  Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu
    1             5             10             15

gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156
Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala
          20             25             30

ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct gtg 204
Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val
          35             40             45

gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg gtg 252
Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val
          50             55             60

tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac tac 300
Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr
          65             70             75

tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt gga 348
Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly
          80             85             90             95

atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg ttc 396
Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe
          100             105             110

ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg tgc 444
Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys
          115             120             125

ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac gtg 492
Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val
          130             135             140

gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc cgg 540
Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg
          145             150             155

gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc tcc 588
Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser
          160             165             170             175

ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc aat 636

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21/28

Leu	Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	Asn	
				180					185					190		
ggg	tcc	ctg	gtc	cca	ggg	tcg	gcc	acc	tgt	acg	gtc	atc	aag	ccc	atg	684
Gly	Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	Pro	Met	
			195					200					205			
tgg	atc	tac	aat	ttc	atc	atc	cag	gtc	acc	tcc	ttc	cta	ttc	tac	ctc	732
Trp	Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	Tyr	Leu	
		210					215					220				
ctc	ccc	atg	act	gtc	atc	agt	gtc	ctc	tac	tac	ctc	atg	gca	ctc	aga	780
Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	Arg	
	225					230					235					
cta	aag	aaa	gac	aaa	tct	ctt	gag	gca	gat	gaa	ggg	aat	gca	aat	att	828
Leu	Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala	Asn	Ile	
240					245					250					255	
caa	aga	ccc	tgc	aga	aaa	tca	gtc	aac	aag	atg	ctg	tct	ttg	tgg	agg	876
Gln	Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Ser	Leu	Trp	Arg	
				260					265					270		
agt	gga	gtg	aat	ccc	tgg	ctg	ctg	tgt	tca	acc	tcg	tcc	atg	tgg	tgt	924
Ser	Gly	Val	Asn	Pro	Trp	Leu	Leu	Cys	Ser	Thr	Ser	Ser	Met	Trp	Cys	
			275					280					285			
cag	gtg	tct	tct	tct	acc	tgagctcagc	tgtcaacccc	attatctata								972
Gln	Val	Ser	Ser	Ser	Thr											
			290													
acctactgtc	tcgcccgttc	caggcagcat	tccagaatgt	gatctcttct	ttccacaaac											1032
agtggcactc	ccagcatgac	ccacagttgc	cacctgccc	gcggaacatc	ttcctgacag											1092
aatgccactt	tgtggagctg	accgaagata	taggtcccca	attcccatgt	cagtcaccca											1152
tgcacaactc	tcacctccca	acagccctct	ctagtgaaca	gatgtcaaga	acaaactatc											1212
aaagcttcca	ctttaacaaa	acctgaattc	tttcagagct	gactctcctc	tatgcctcaa											1272
aacttcagag	aggaacatcc	cataatgtat	gccttctcat	atgatattag	agaggtagaa											1332
tggctcttac	aactcatgta	ccatttgcta	gttttttttt	tttaataaac	gtgaaaactg											1392
agagttagat	ctggtttcaa	aaccaagac	tgccctgattt	ttagttatct	ttccactatc											1452
ctaactgcct	catgcccctt	cactagttca	tgccaagaac	gtgactggaa	aggcatggca											1512
cctatacctt	gattaatttc	cattaatgga	aatgggttcgt	cctgagtcac	ctacgttccg											1572
agtcaggctg	tcactcctac	ta														1594

&lt;210&gt; 12

&lt;211&gt; 293

22/28

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

Met	Glu	Lys	Leu	Gln	Asn	Ala	Ser	Trp	Ile	Tyr	Gln	Gln	Lys	Leu	Glu	1	5	10	15
Asp	Pro	Phe	Gln	Lys	His	Leu	Asn	Ser	Thr	Glu	Glu	Tyr	Leu	Ala	Phe	20	25	30	
Leu	Cys	Gly	Pro	Arg	Arg	Ser	His	Phe	Phe	Leu	Pro	Val	Ser	Val	Val	35	40	45	
Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val	Leu	Val	Cys	50	55	60	
Leu	Val	Ile	Leu	Gln	His	Gln	Ala	Met	Lys	Thr	Pro	Thr	Asn	Tyr	Tyr	65	70	75	80
Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu	Leu	Gly	Met	85	90	95	
Pro	Leu	Glu	Val	Tyr	Glu	Met	Trp	Arg	Asn	Tyr	Pro	Phe	Leu	Phe	Gly	100	105	110	
Pro	Val	Gly	Cys	Tyr	Phe	Lys	Thr	Ala	Leu	Phe	Glu	Thr	Val	Cys	Phe	115	120	125	
Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg	Tyr	Val	Ala	130	135	140	
Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg	Arg	Ala	145	150	155	160
Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu	Phe	Ser	Leu	165	170	175	
Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	Asn	Gly	180	185	190	
Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	Pro	Met	Trp	195	200	205	
Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	Tyr	Leu	Leu	210	215	220	
Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	Arg	Leu	225	230	235	240
Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala	Asn	Ile	Gln	245	250	255	
Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Ser	Leu	Trp	Arg	Ser	260	265	270	
Gly	Val	Asn	Pro	Trp	Leu	Leu	Cys	Ser	Thr	Ser	Ser	Met	Trp	Cys	Gln				

23/28

275

280

285

Val Ser Ser Ser Thr  
290

<210> 13  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Degenerated  
primers

<220>  
<221> variation  
<222> (21)  
<223> A,C,G or T

<220>  
<221> variation  
<222> (24)  
<223> A, C, G or T

<400> 13  
ctcatcttcg cgggtgggcrc ngynngg

26

<210> 14  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Degenerated  
primers

<220>  
<221> variation  
<222> (22)  
<223> C or Inosine

<220>  
<221> variation  
<222> (25)  
<223> A, C, G or T

<220>  
<221> variation  
<222> (28)  
<223> A, C, G or T

<400> 14  
ggccaggcag cgctccgcgc tnarncyngc d

31

24/28

<210> 15  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Degenerated  
primers

<400> 15  
gaartartag ccrcgrcagc cw 22

<210> 16  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

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<220>  
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25/28

&lt;220&gt;

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&lt;400&gt; 19

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

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29

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

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30

&lt;210&gt; 22

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Degenerated primers

&lt;400&gt; 22

cggaagttgg cggacacgrv rttrta

26

&lt;210&gt; 23

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 23

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26/28

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27/28

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 29

tagtaggagt gacagcctga ctcggaacg

29

&lt;210&gt; 30

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 30

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30

&lt;210&gt; 31

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 31

tcgtaccagg ggaggctcag gc

22

&lt;210&gt; 32

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 32

cctcttcagc ctggcggtct ctg

23

&lt;210&gt; 33

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

28/28

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 33

ggaggcgaag cacacgggtct ca

22

&lt;210&gt; 34

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; (1)

&lt;223&gt; Labeled with 6-carboxyfluorescein

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; (34)

&lt;223&gt; Labeled with

N,N,N',N'-tetramethyl-6-carboxyrhodamin

&lt;400&gt; 34

agatgtggcg caactaccct ttcttggttcg ggcc

34

10/088744

Rec'd PCT/PTO 22 JUL 2002

## SEQUENCE LISTING

&lt;110&gt; SOLVAY PHARMACEUTICALS B.V.

&lt;120&gt; Novel human G-protein coupled Receptor

&lt;130&gt; SPW99.06/HA 00.19

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 34

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1658

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (55)..(1299)

&lt;223&gt; IGS4A long version

&lt;400&gt; 1

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Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys
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cta gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg 153
Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu
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Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser
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Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn
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Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu
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Leu	Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	
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Val	Leu	Val	Phe	Ala	Ile	Cys	Trp	Ala	Pro	Phe	His	Ile	Asp	Arg	Leu	
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Phe	Phe	Ser	Phe	Val	Glu	Glu	Trp	Ser	Glu	Ser	Leu	Ala	Ala	Val	Phe	
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gac cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc 1161  
Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys  
355 360 365

cac ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cca tgt cag 1209  
His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys Gln  
370 375 380 385

tca tcc atg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag 1257  
Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln  
390 395 400

atg tca aga aca aac tat caa agc ttc cac ttt aac aaa acc 1299  
Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr  
405 410 415

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Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val  
35 40 45  
Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val  
50 55 60  
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65 70 75 80  
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<222> (64)..(1299)
<223> IGS4A short version
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 Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu  
 1 5 10 15

gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156  
Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala  
20 25 30

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Phe	Leu	Cys	Gly	Pro	Arg	Arg	Ser	His	Phe	Phe	Leu	Pro	Val	Ser	Val	
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Val	Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val	Leu	Val	
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Cys	Leu	Val	Ile	Leu	Gln	His	Gln	Ala	Met	Lys	Thr	Pro	Thr	Asn	Tyr	
	65					70					75					

tac	ctc	ttc	agc	ctg	gcg	gtc	tct	gac	ctc	ctg	gtc	ctg	ctc	ctt	gga	348
Tyr	Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu	Leu	Gly	
80					85					90					95	

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130 135 140

gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc cgg 540  
Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg  
145 150 155



gcc Ala 160	ctc Leu	agg Arg	atc Ile	ctc Leu	ggc Gly 165	atc Ile	gtc Val	tgg Trp	ggc Gly	ttc Phe 170	tcc Ser	gtg Val	ctc Leu	ttc Phe	tcc Ser 175	588
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cca Pro	cag Gln	ttg Leu	cca Pro 355	cct Pro	gcc Ala	cag Gln	cgg Arg	aac Asn 360	atc Ile	ttc Phe	ctg Leu	aca Thr	gaa Glu 365	tgc Cys	cac His	1164
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Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr
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Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe
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tcc ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc 633
Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro
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Leu	Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	
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Ile	Gln	Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Phe	Val	Leu	
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Ser	Ser	Val	His	Asn	Ser	His	Leu	Pro	Thr	Ala	Leu	Ser	Ser	Glu	Gln	
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Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val				
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Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg				
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Leu Phe Phe Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val				
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Phe Asn Leu Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser				
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Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln				
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His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu				
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Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys				
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Ala	Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg	Arg	
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Pro	Val	Gly 115	Cys	Tyr	Phe	Lys	Thr 120	Ala	Leu	Phe	Glu	Thr 125	Val	Cys	Phe
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Lys	Lys	Asp	Lys	Ser 245	Leu	Glu	Ala	Asp	Glu 250	Gly	Asn	Ala	Asn	Ile 255	Gln
Arg	Pro	Cys	Arg 260	Lys	Ser	Val	Asn	Lys 265	Met	Leu	Phe	Val	Leu 270	Val	Leu
Val	Phe	Ala	Ile	Cys	Trp	Ala	Pro	Phe	His	Ile	Asp	Arg	Leu	Phe	Phe

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

275		280		285
Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val Phe Asn Leu				
290		295		300
Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser Ala Val Asn				
305		310		315
Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala Phe Gln				
		325		330
Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His Asp Pro				
		340		345
Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys His Phe				
		355		360
Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys Gln Ser Ser				
		370		375
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Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr				
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Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys		
	5	10
		15
cta gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg	153	
Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu		
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		30
gcc ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct	201	
Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser		
	35	40
		45
gtg gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg	249	
Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu		



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tgt cag gtg tct tct tct acc tgagctcagc tgtcaacccc attatctata 972  
Cys Gln Val Ser Ser Ser Thr  
290 295

acctactgtc tcgccgcttc caggcagcat tccagaatgt gatctcttct tccacaaaac 1032  
agtggcactc ccagcatgac ccacagttgc cacctgcccac gcggaacatc ttcctgacag 1092  
aatgccactt tgtggagctg accgaagata taggtcccca attcccatgt cagtcaccca 1152  
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agagtttagat ctggtttcaa aaccaagac tgccatgatt ttagttatct tccactatc 1452  
ctaactgcct catgcccctt cactagttca tgccaagaac gtgactggaa aggcattggc 1512  
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Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val  
35 40 45  
Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val  
50 55 60  
Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr  
65 70 75 80  
Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu  
85 90 95  
Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe  
100 105 110  
Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr  
115 120 125

Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg  
130 135 140

Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg  
145 150 155 160

Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu  
165 170 175

Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe  
180 185 190

Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys  
195 200 205

Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe  
210 215 220

Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala  
225 230 235 240

Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala  
245 250 255

Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu  
260 265 270

Trp Arg Ser Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met  
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Trp Cys Gln Val Ser Ser Ser Thr  
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ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa cta 108  
Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu  
1 5 10 15

gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156  
Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala  
20 25 30

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

ttc	ctc	tgc	gga	cct	cgg	cgc	agc	cac	ttc	ttc	ctc	ccc	gtg	tct	gtg	204
Phe	Leu	Cys	Gly	Pro	Arg	Arg	Ser	His	Phe	Phe	Leu	Pro	Val	Ser	Val	
			35					40					45			
gtg	tat	gtg	cca	att	ttt	gtg	gtg	ggg	gtc	att	ggc	aat	gtc	ctg	gtg	252
Val	Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val	Leu	Val	
		50					55					60				
tgc	ctg	gtg	att	ctg	cag	cac	cag	gct	atg	aag	acg	ccc	acc	aac	tac	300
Cys	Leu	Val	Ile	Leu	Gln	His	Gln	Ala	Met	Lys	Thr	Pro	Thr	Asn	Tyr	
	65					70					75					
tac	ctc	ttc	agc	ctg	gcg	gtc	tct	gac	ctc	ctg	gtc	ctg	ctc	ctt	gga	348
Tyr	Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu	Leu	Gly	
	80				85				90						95	
atg	ccc	ctg	gag	gtc	tat	gag	atg	tgg	cgc	aac	tac	cct	ttc	ttg	ttc	396
Met	Pro	Leu	Glu	Val	Tyr	Glu	Met	Trp	Arg	Asn	Tyr	Pro	Phe	Leu	Phe	
			100					105						110		
ggg	ccc	gtg	ggc	tgc	tac	ttc	aag	acg	gcc	ctc	ttt	gag	acc	gtg	tgc	444
Gly	Pro	Val	Gly	Cys	Tyr	Phe	Lys	Thr	Ala	Leu	Phe	Glu	Thr	Val	Cys	
			115					120					125			
ttc	gcc	tcc	atc	ctc	agc	atc	acc	acc	gtc	agc	gtg	gag	cgc	tac	gtg	492
Phe	Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg	Tyr	Val	
		130					135					140				
gcc	atc	cta	cac	ccg	ttc	cgc	gcc	aaa	ctg	cag	agc	acc	cgg	cgc	cgg	540
Ala	Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg	Arg	
	145					150					155					
gcc	ctc	agg	atc	ctc	ggc	atc	gtc	tgg	ggc	ttc	tcc	gtg	ctc	ttc	tcc	588
Ala	Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu	Phe	Ser	
	160				165					170					175	
ctg	ccc	aac	acc	agc	atc	cat	ggc	atc	aag	ttc	cac	tac	ttc	ccc	aat	636
Leu	Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	Asn	
				180					185					190		
ggg	tcc	ctg	gtc	cca	ggg	tgc	gcc	acc	tgt	acg	gtc	atc	aag	ccc	atg	684
Gly	Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	Pro	Met	
			195					200					205			
tgg	atc	tac	aat	ttc	atc	atc	cag	gtc	acc	tcc	ttc	cta	ttc	tac	ctc	732
Trp	Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	Tyr	Leu	
		210					215					220				
ctc	ccc	atg	act	gtc	atc	agt	gtc	ctc	tac	tac	ctc	atg	gca	ctc	aga	780
Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	Arg	
	225					230					235					
cta	aag	aaa	gac	aaa	tct	ctt	gag	gca	gat	gaa	ggg	aat	gca	aat	att	828
Leu	Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala	Asn	Ile	
	240				245					250					255	
caa	aga	ccc	tgc	aga	aaa	tca	gtc	aac	aag	atg	ctg	tct	ttg	tgg	agg	876

Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu Trp Arg  
 260 265 270

agt gga gtg aat ccc tgg ctg ctg tgt tca acc tcg tcc atg tgg tgt 924  
 Ser Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met Trp Cys  
 275 280 285

cag gtg tct tct tct acc tgagctcagc tgtcaacccc attatctata 972  
 Gln Val Ser Ser Ser Thr  
 290

acctactgtc tcgcccgttc caggcagcat tccagaatgt gatctcttct ttccacaaac 1032  
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 aatgccactt tgtggagctg accgaagata taggtcccca attcccatgt cagtcattcca 1152  
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 Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val Val  
 35 40 45  
 Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val Cys  
 50 55 60  
 Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr Tyr  
 65 70 75 80  
 Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly Met  
 85 90 95



.. .. .

Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe Gly  
100 105 110

Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys Phe  
115 120 125

Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val Ala  
130 135 140

Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg Ala  
145 150 155 160

Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser Leu  
165 170 175

Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn Gly  
180 185 190

Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met Trp  
195 200 205

Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu Leu  
210 215 220

Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg Leu  
225 230 235 240

Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile Gln  
245 250 255

Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu Trp Arg Ser  
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Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met Trp Cys Gln  
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Val Ser Ser Ser Thr  
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primers

<220>  
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<222> (21)  
<223> A,C,G or T

<220>



will be used to generate a library of 1000 clones. The library will be screened for clones that express the protein of interest. The clones that express the protein of interest will be identified and the protein will be purified. The purified protein will be used for structural analysis.

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27

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23

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29

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26

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27

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<212> DNA  
<213> Artificial Sequence

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<222> (34)
<223> Labeled with
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1/28

## SEQUENCE LISTING

&lt;110&gt; SOLVAY PHARMACEUTICALS B.V.

&lt;120&gt; Novel human G-protein coupled Receptor

&lt;130&gt; SPW99.06/HA 00.19

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 34

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1658

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (55)..(1299)

&lt;223&gt; IGS4A long version

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                                     1

tca ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa 105
Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys
          5                      10                      15

cta gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg 153
Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu
          20                      25                      30

gcc ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct 201
Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser
          35                      40                      45

gtg gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg 249
Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu
          50                      55                      60                      65

gtg tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac 297
Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn
          70                      75                      80

tac tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt 345
Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu
          85                      90                      95

gga atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg 393
Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu

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2/28

100	105	110	
ttc ggg ccc gtg ggc tgc tac	ttc aag acg gcc ctc	ttt gag acc gtg	441
Phe Gly Pro Val Gly Cys Tyr	Phe Lys Thr Ala Leu	Phe Glu Thr Val	
115	120	125	
tgc ttc gcc tcc atc ctc agc	atc acc acc gtc agc	gtg gag cgc tac	489
Cys Phe Ala Ser Ile Leu	Ser Ile Thr Thr Val	Ser Val Glu Arg Tyr	
130	135	140 145	
gtg gcc atc cta cac ccg ttc	cgc gcc aaa ctg cag	agc acc cgg cgc	537
Val Ala Ile Leu His Pro	Phe Arg Ala Lys Leu	Gln Ser Thr Arg Arg	
150	155	160	
cgg gcc ctc agg atc ctc ggc	atc gtc tgg ggc ttc	tcc gtg ctc ttc	585
Arg Ala Leu Arg Ile Leu	Gly Ile Val Trp Gly	Phe Ser Val Leu Phe	
165	170	175	
tcc ctg ccc aac acc agc atc	cat ggc atc aag ttc	cac tac ttc ccc	633
Ser Leu Pro Asn Thr Ser	Ile His Gly Ile Lys	Phe His Tyr Phe Pro	
180	185	190	
aat ggg tcc ctg gtc cca ggt	tgc gcc acc tgt acg	gtc atc aag ccc	681
Asn Gly Ser Leu Val Pro	Gly Ser Ala Thr Cys	Thr Val Ile Lys Pro	
195	200	205	
atg tgg atc tac aat ttc	atc atc cag gtc acc	tcc ttc cta ttc tac	729
Met Trp Ile Tyr Asn Phe	Ile Ile Gln Val Thr	Ser Phe Leu Phe Tyr	
210	215	220 225	
ctc ctc ccc atg act gtc	atc agt gtc ctc tac	tac ctc atg gca ctc	777
Leu Leu Pro Met Thr Val	Ile Ser Val Leu Tyr	Tyr Leu Met Ala Leu	
230	235	240	
aga cta aag aaa gac aaa	tct ctt gag gca gat	gaa ggg aat gca aat	825
Arg Leu Lys Lys Asp Lys	Ser Leu Glu Ala Asp	Glu Gly Asn Ala Asn	
245	250	255	
att caa aga ccc tgc aga	aaa tca gtc aac aag	atg ctg ttt gtc ttg	873
Ile Gln Arg Pro Cys Arg	Lys Ser Val Asn Lys	Met Leu Phe Val Leu	
260	265	270	
gtc tta gtg ttt gct atc	tgt tgg gcc ccg ttc	cac att gac cga ctc	921
Val Leu Val Phe Ala Ile	Cys Trp Ala Pro Phe	His Ile Asp Arg Leu	
275	280	285	
ttc ttc agc ttt gtg gag	gag tgg agt gaa tcc	ctg gct gct gtg ttc	969
Phe Phe Ser Phe Val Glu	Glu Trp Ser Glu Ser	Leu Ala Ala Val Phe	
290	295	300 305	
aac ctc gtc cat gtg gtg	tca ggt gtc ttc ttc	tac ctg agc tca gct	1017
Asn Leu Val His Val Val	Ser Gly Val Phe Phe	Tyr Leu Ser Ser Ala	
310	315	320	
gtc aac ccc att atc tat	aac cta ctg tct cgc	cgc ttc cag gca gca	1065
Val Asn Pro Ile Ile Tyr	Asn Leu Leu Ser Arg	Arg Phe Gln Ala Ala	

3/28

325	330	335	
ttc cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat			1113
Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His			
340	345	350	
gac cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc			1161
Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys			
355	360	365	
cac ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cca tgt cag			1209
His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys Gln			
370	375	380	385
tca tcc atg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag			1257
Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln			
390	395	400	
atg tca aga aca aac tat caa agc ttc cac ttt aac aaa acc			1299
Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr			
405	410	415	
tgaattcttt cagagctgac tctcctctat gcctcaaaac ttcagagagg aacatcccat			1359
aatgtatgcc ttctcatatg atattagaga ggtagaatgg ctcttacaac tcatgtaccc			1419
attgctagtt tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac			1479
ccaagactgc ctgattttta gttatctttc cactatccta actgcctcat gcccttcac			1539
tagttcatgc caagaacgtg actggaaagg catggcacct ataccttgat taatttccat			1599
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Met Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln			
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Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr			
20	25	30	
Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val			
35	40	45	
Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val			
50	55	60	
Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr			
65	70	75	80

4/28

Asn	Tyr	Tyr	Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu	85	90	95	
Leu	Gly	Met	Pro	Leu	Glu	Val	Tyr	Glu	Met	Trp	Arg	Asn	Tyr	Pro	Phe	100	105	110	
Leu	Phe	Gly	Pro	Val	Gly	Cys	Tyr	Phe	Lys	Thr	Ala	Leu	Phe	Glu	Thr	115	120	125	
Val	Cys	Phe	Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg	130	135	140	
Tyr	Val	Ala	Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	145	150	155	160
Arg	Arg	Ala	Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu	165	170	175	
Phe	Ser	Leu	Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	180	185	190	
Pro	Asn	Gly	Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	195	200	205	
Pro	Met	Trp	Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	210	215	220	
Tyr	Leu	Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	225	230	235	240
Leu	Arg	Leu	Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala	245	250	255	
Asn	Ile	Gln	Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Phe	Val	260	265	270	
Leu	Val	Leu	Val	Phe	Ala	Ile	Cys	Trp	Ala	Pro	Phe	His	Ile	Asp	Arg	275	280	285	
Leu	Phe	Phe	Ser	Phe	Val	Glu	Glu	Trp	Ser	Glu	Ser	Leu	Ala	Ala	Val	290	295	300	
Phe	Asn	Leu	Val	His	Val	Val	Ser	Gly	Val	Phe	Phe	Tyr	Leu	Ser	Ser	305	310	315	320
Ala	Val	Asn	Pro	Ile	Ile	Tyr	Asn	Leu	Leu	Ser	Arg	Arg	Phe	Gln	Ala	325	330	335	
Ala	Phe	Gln	Asn	Val	Ile	Ser	Ser	Phe	His	Lys	Gln	Trp	His	Ser	Gln	340	345	350	
His	Asp	Pro	Gln	Leu	Pro	Pro	Ala	Gln	Arg	Asn	Ile	Phe	Leu	Thr	Glu	355	360	365	
Cys	His	Phe	Val	Glu	Leu	Thr	Glu	Asp	Ile	Gly	Pro	Gln	Phe	Pro	Cys	370	375	380	

5/28

Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu  
 385 390 395 400

Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr  
 405 410 415

<210> 3  
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 Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu  
 1 5 10 15  
 gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156  
 Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala  
 20 25 30  
 ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct gtg 204  
 Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val  
 35 40 45  
 gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg gtg 252  
 Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val  
 50 55 60  
 tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac tac 300  
 Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr  
 65 70 75  
 tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt gga 348  
 Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly  
 80 85 90 95  
 atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg ttc 396  
 Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe  
 100 105 110  
 ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg tgc 444  
 Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys  
 115 120 125  
 ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac gtg 492  
 Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val

6/28

130					135					140							
gcc	atc	cta	cac	ccg	ttc	cgc	gcc	aaa	ctg	cag	agc	acc	cgg	cgc	cgg	540	
Ala	Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg	Arg		
145					150					155							
gcc	ctc	agg	atc	ctc	ggc	atc	gtc	tgg	ggc	ttc	tcc	gtg	ctc	ttc	tcc	588	
Ala	Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu	Phe	Ser		
160					165					170					175		
ctg	ccc	aac	acc	agc	atc	cat	ggc	atc	aag	ttc	cac	tac	ttc	ccc	aat	636	
Leu	Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	Asn		
180					185					190							
ggg	tcc	ctg	gtc	cca	ggg	tcg	gcc	acc	tgt	acg	gtc	atc	aag	ccc	atg	684	
Gly	Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	Pro	Met		
195					200					205							
tgg	atc	tac	aat	ttc	atc	atc	cag	gtc	acc	tcc	ttc	cta	ttc	tac	ctc	732	
Trp	Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	Tyr	Leu		
210					215					220							
ctc	ccc	atg	act	gtc	atc	agt	gtc	ctc	tac	tac	ctc	atg	gca	ctc	aga	780	
Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	Arg		
225					230					235							
cta	aag	aaa	gac	aaa	tct	ctt	gag	gca	gat	gaa	ggg	aat	gca	aat	att	828	
Leu	Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala	Asn	Ile		
240					245					250					255		
caa	aga	ccc	tgc	aga	aaa	tca	gtc	aac	aag	atg	ctg	ttt	gtc	ttg	gtc	876	
Gln	Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Phe	Val	Leu	Val		
260					265					270							
tta	gtg	ttt	gct	atc	tgt	tgg	gcc	ccg	ttc	cac	att	gac	cga	ctc	ttc	924	
Leu	Val	Phe	Ala	Ile	Cys	Trp	Ala	Pro	Phe	His	Ile	Asp	Arg	Leu	Phe		
275					280					285							
ttc	agc	ttt	gtg	gag	gag	tgg	agt	gaa	tcc	ctg	gct	gct	gtg	ttc	aac	972	
Phe	Ser	Phe	Val	Glu	Glu	Trp	Ser	Glu	Ser	Leu	Ala	Ala	Val	Phe	Asn		
290					295					300							
ctc	gtc	cat	gtg	gtg	tca	ggg	gtc	ttc	ttc	tac	ctg	agc	tca	gct	gtc	1020	
Leu	Val	His	Val	Val	Ser	Gly	Val	Phe	Phe	Tyr	Leu	Ser	Ser	Ala	Val		
305					310					315							
aac	ccc	att	atc	tat	aac	cta	ctg	tct	cgc	cgc	ttc	cag	gca	gca	ttc	1068	
Asn	Pro	Ile	Ile	Tyr	Asn	Leu	Leu	Ser	Arg	Arg	Phe	Gln	Ala	Ala	Phe		
320					325					330					335		
cag	aat	gtg	atc	tct	tct	ttc	cac	aaa	cag	tgg	cac	tcc	cag	cat	gac	1116	
Gln	Asn	Val	Ile	Ser	Ser	Phe	His	Lys	Gln	Trp	His	Ser	Gln	His	Asp		
340					345					350							
cca	cag	ttg	cca	cct	gcc	cag	cgg	aac	atc	ttc	ctg	aca	gaa	tgc	cac	1164	
Pro	Gln	Leu	Pro	Pro	Ala	Gln	Arg	Asn	Ile	Phe	Leu	Thr	Glu	Cys	His		

7/28

355 360 365  
 ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cca tgt cag tca 1212  
 Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys Gln Ser  
 370 375 380  
 tcc atg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag atg 1260  
 Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln Met  
 385 390 395  
 tca aga aca aac tat caa agc ttc cac ttt aac aaa acc tgaattcttt 1309  
 Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr  
 400 405 410  
 cagagctgac tctcctctat gcctcaaaac ttcagagagg aacatcccat aatgtatgcc 1369  
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 tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac ccaagactgc 1489  
 ctgatttttta gttatctttc cactatccta actgcctcat gcccttcac tagttcatgc 1549  
 caagaacgtg actggaaagg catggcacct ataccttgat taatttccat taatggaaat 1609  
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 20 25 30  
 Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val Val  
 35 40 45  
 Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val Cys  
 50 55 60  
 Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr Tyr  
 65 70 75 80  
 Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly Met  
 85 90 95  
 Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe Gly  
 100 105 110  
 Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys Phe  
 115 120 125

8/28

Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg	Tyr	Val	Ala	130	135	140
Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg	Arg	Ala	145	150	155
Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu	Phe	Ser	Leu	165	170	175
Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	Asn	Gly	180	185	190
Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	Pro	Met	Trp	195	200	205
Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	Tyr	Leu	Leu	210	215	220
Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	Arg	Leu	225	230	235
Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala	Asn	Ile	Gln	245	250	255
Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Phe	Val	Leu	Val	Leu	260	265	270
Val	Phe	Ala	Ile	Cys	Trp	Ala	Pro	Phe	His	Ile	Asp	Arg	Leu	Phe	Phe	275	280	285
Ser	Phe	Val	Glu	Glu	Trp	Ser	Glu	Ser	Leu	Ala	Ala	Val	Phe	Asn	Leu	290	295	300
Val	His	Val	Val	Ser	Gly	Val	Phe	Phe	Tyr	Leu	Ser	Ser	Ala	Val	Asn	305	310	315
Pro	Ile	Ile	Tyr	Asn	Leu	Leu	Ser	Arg	Arg	Phe	Gln	Ala	Ala	Phe	Gln	325	330	335
Asn	Val	Ile	Ser	Ser	Phe	His	Lys	Gln	Trp	His	Ser	Gln	His	Asp	Pro	340	345	350
Gln	Leu	Pro	Pro	Ala	Gln	Arg	Asn	Ile	Phe	Leu	Thr	Glu	Cys	His	Phe	355	360	365
Val	Glu	Leu	Thr	Glu	Asp	Ile	Gly	Pro	Gln	Phe	Pro	Cys	Gln	Ser	Ser	370	375	380
Met	His	Asn	Ser	His	Leu	Pro	Thr	Ala	Leu	Ser	Ser	Glu	Gln	Met	Ser	385	390	395
Arg	Thr	Asn	Tyr	Gln	Ser	Phe	His	Phe	Asn	Lys	Thr					405	410	

9/28

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tca ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa 105  
 Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys  
 5 10 15

cta gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg 153  
 Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu  
 20 25 30

gcc ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct 201  
 Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser  
 35 40 45

gtg gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg 249  
 Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu  
 50 55 60 65

gtg tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac 297  
 Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn  
 70 75 80

tac tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt 345  
 Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu  
 85 90 95

gga atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg 393  
 Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu  
 100 105 110

ttc ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg 441  
 Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val  
 115 120 125

tgc ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac 489  
 Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr  
 130 135 140 145

gtg gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc 537  
 Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg  
 150 155 160



10/28

cgg gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc	585
Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe	
165 170 175	
tcc ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc	633
Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro	
180 185 190	
aat ggg tcc ctg gtc cca ggt tcg gcc acc tgt acg gtc atc aag ccc	681
Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro	
195 200 205	
atg tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac	729
Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr	
210 215 220 225	
ctc ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc	777
Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu	
230 235 240	
aga cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat	825
Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn	
245 250 255	
att caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg	873
Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu	
260 265 270	
gtc tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc	921
Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu	
275 280 285	
ttc ttc agc ttt gtg gag gag tgg act gaa tcc ctg gct gct gtg ttc	969
Phe Phe Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val Phe	
290 295 300 305	
aac ctc gtc cat gtg gtg tca ggt gtc tta ttc tac ctg agc tca gct	1017
Asn Leu Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser Ala	
310 315 320	
gtc aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca	1065
Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala	
325 330 335	
ttc cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat	1113
Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His	
340 345 350	
gac cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc	1161
Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys	
355 360 365	
cac ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cta tgt cag	1209
His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys Gln	
370 375 380 385	

11/28

tca tcc gtg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag 1257  
 Ser Ser Val His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln  
                     390                    395                    400

atg tca aga aca aac tat caa agc ttc cac ttt aac aaa acc 1299  
 Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr  
                     405                    410                    415

tgaattcttt cagagctgac tctcctctat gcctcaaaac ttcagagagg aacatcccat 1359  
 aatgtatgcc ttctcatatg aaattagaga ggtagaatgg ctcttacaac tcatgtaccc 1419  
 attgctagtt tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac 1479  
 ccaagactgc ctgattttta gttatctttc cactatccta actgcctcat gccccttcac 1539  
 tagttcatgc caagaacgtg actggaaagg catggcacct ataccttgat taatttccat 1599  
 taatggaaat gggtcgtcct gagtcaccta cgttccgagt caggctgtca ctectacta 1658

<210> 6  
 <211> 415  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Met Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln  
   1                    5                    10                    15  
 Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr  
                     20                    25                    30  
 Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val  
                     35                    40                    45  
 Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val  
                     50                    55                    60  
 Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr  
   65                    70                    75                    80  
 Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu  
                     85                    90                    95  
 Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe  
                     100                    105                    110  
 Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr  
                     115                    120                    125  
 Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg  
                     130                    135                    140  
 Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg  
  145                    150                    155                    160

12/28

Arg	Arg	Ala	Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu
			165						170					175	
Phe	Ser	Leu	Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe
			180					185					190		
Pro	Asn	Gly	Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys
		195					200					205			
Pro	Met	Trp	Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe
	210					215					220				
Tyr	Leu	Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala
225					230					235					240
Leu	Arg	Leu	Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala
			245						250					255	
Asn	Ile	Gln	Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Phe	Val
			260					265					270		
Leu	Val	Leu	Val	Phe	Ala	Ile	Cys	Trp	Ala	Pro	Phe	His	Ile	Asp	Arg
	275						280					285			
Leu	Phe	Phe	Ser	Phe	Val	Glu	Glu	Trp	Thr	Glu	Ser	Leu	Ala	Ala	Val
	290					295					300				
Phe	Asn	Leu	Val	His	Val	Val	Ser	Gly	Val	Leu	Phe	Tyr	Leu	Ser	Ser
305					310					315					320
Ala	Val	Asn	Pro	Ile	Ile	Tyr	Asn	Leu	Leu	Ser	Arg	Arg	Phe	Gln	Ala
			325					330						335	
Ala	Phe	Gln	Asn	Val	Ile	Ser	Ser	Phe	His	Lys	Gln	Trp	His	Ser	Gln
			340					345					350		
His	Asp	Pro	Gln	Leu	Pro	Pro	Ala	Gln	Arg	Asn	Ile	Phe	Leu	Thr	Glu
		355					360					365			
Cys	His	Phe	Val	Glu	Leu	Thr	Glu	Asp	Ile	Gly	Pro	Gln	Phe	Leu	Cys
	370					375					380				
Gln	Ser	Ser	Val	His	Asn	Ser	His	Leu	Pro	Thr	Ala	Leu	Ser	Ser	Glu
385					390					395					400
Gln	Met	Ser	Arg	Thr	Asn	Tyr	Gln	Ser	Phe	His	Phe	Asn	Lys	Thr	
			405						410					415	

&lt;210&gt; 7

&lt;211&gt; 1658

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

13/28

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (64)..(1299)

&lt;223&gt; IGS4B short version

&lt;400&gt; 7

ggctcagctt gaaacagagc ctcgtaccag gggaggctca ggccttggat tttaatgtca 60

ggg	atg	gaa	aaa	ctt	cag	aat	gct	tcc	tgg	atc	tac	cag	cag	aaa	cta	108
Met	Glu	Lys	Leu	Gln	Asn	Ala	Ser	Trp	Ile	Tyr	Gln	Gln	Lys	Leu		
1				5					10					15		

gaa	gat	cca	ttc	cag	aaa	cac	ctg	aac	agc	acc	gag	gag	tat	ctg	gcc	156
Glu	Asp	Pro	Phe	Gln	Lys	His	Leu	Asn	Ser	Thr	Glu	Glu	Tyr	Leu	Ala	
			20					25						30		

ttc	ctc	tgc	gga	cct	cgg	cgc	agc	cac	ttc	ttc	ctc	ccc	gtg	tct	gtg	204
Phe	Leu	Cys	Gly	Pro	Arg	Arg	Ser	His	Phe	Phe	Leu	Pro	Val	Ser	Val	
		35					40						45			

gtg	tat	gtg	cca	att	ttt	gtg	gtg	ggg	gtc	att	ggc	aat	gtc	ctg	gtg	252
Val	Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val	Leu	Val	
		50					55					60				

tgc	ctg	gtg	att	ctg	cag	cac	cag	gct	atg	aag	acg	ccc	acc	aac	tac	300
Cys	Leu	Val	Ile	Leu	Gln	His	Gln	Ala	Met	Lys	Thr	Pro	Thr	Asn	Tyr	
	65					70					75					

tac	ctc	ttc	agc	ctg	gcg	gtc	tct	gac	ctc	ctg	gtc	ctg	ctc	ctt	gga	348
Tyr	Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu	Leu	Gly	
80					85					90					95	

atg	ccc	ctg	gag	gtc	tat	gag	atg	tgg	cgc	aac	tac	cct	ttc	ttg	ttc	396
Met	Pro	Leu	Glu	Val	Tyr	Glu	Met	Trp	Arg	Asn	Tyr	Pro	Phe	Leu	Phe	
			100					105						110		

ggg	ccc	gtg	ggc	tgc	tac	ttc	aag	acg	gcc	ctc	ttt	gag	acc	gtg	tgc	444
Gly	Pro	Val	Gly	Cys	Tyr	Phe	Lys	Thr	Ala	Leu	Phe	Glu	Thr	Val	Cys	
		115						120					125			

ttc	gcc	tcc	atc	ctc	agc	atc	acc	acc	gtc	agc	gtg	gag	cgc	tac	gtg	492
Phe	Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg	Tyr	Val	
		130					135					140				

gcc	atc	cta	cac	ccg	ttc	cgc	gcc	aaa	ctg	cag	agc	acc	cgg	cgc	cgg	540
Ala	Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg	Arg	
	145					150					155					

gcc	ctc	agg	atc	ctc	ggc	atc	gtc	tgg	ggc	ttc	tcc	gtg	ctc	ttc	tcc	588
Ala	Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu	Phe	Ser	
160					165				170						175	

ctg	ccc	aac	acc	agc	atc	cat	ggc	atc	aag	ttc	cac	tac	ttc	ccc	aat	636
Leu	Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	Asn	
				180					185					190		

14/28

ggg tcc ctg gtc cca ggt tcg gcc acc tgt acg gtc atc aag ccc atg	684
Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met	
195 200 205	
tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac ctc	732
Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu	
210 215 220	
ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc aga	780
Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg	
225 230 235	
cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat att	828
Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile	
240 245 250 255	
caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg gtc	876
Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu Val	
260 265 270	
tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc ttc	924
Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu Phe	
275 280 285	
ttc agc ttt gtg gag gag tgg act gaa tcc ctg gct gct gtg ttc aac	972
Phe Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val Phe Asn	
290 295 300	
ctc gtc cat gtg gtg tca ggt gtc tta ttc tac ctg agc tca gct gtc	1020
Leu Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser Ala Val	
305 310 315	
aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca ttc	1068
Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala Phe	
320 325 330 335	
cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat gac	1116
Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His Asp	
340 345 350	
cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc cac	1164
Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys His	
355 360 365	
ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cta tgt cag tca	1212
Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys Gln Ser	
370 375 380	
tcc gtg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag atg	1260
Ser Val His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln Met	
385 390 395	
tca aga aca aac tat caa agc ttc cac ttt aac aaa acc tgaattcttt	1309
Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr	
400 405 410	

15/28

cagagctgac tctcctctat gcctcaaaac ttcagagagg aacatcccat aatgtatgcc 1369  
 ttctcatatg aaattagaga ggtagaatgg ctcttacaac tcatgtaccc attgctagtt 1429  
 tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac ccaagactgc 1489  
 ctgattttta gttatctttc cactatccta actgcctcat gccctttcac tagttcatgc 1549  
 caagaacgtg actggaaagg catggcacct ataccttgat taatttccat taatggaaat 1609  
 ggttcgtcct gagtcatcta cgttccgagt caggctgtca ctcctacta 1658

&lt;210&gt; 8

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

Met	Glu	Lys	Leu	Gln	Asn	Ala	Ser	Trp	Ile	Tyr	Gln	Gln	Lys	Leu	Glu
1				5					10					15	
Asp	Pro	Phe	Gln	Lys	His	Leu	Asn	Ser	Thr	Glu	Glu	Tyr	Leu	Ala	Phe
			20					25					30		
Leu	Cys	Gly	Pro	Arg	Arg	Ser	His	Phe	Phe	Leu	Pro	Val	Ser	Val	Val
		35					40					45			
Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val	Leu	Val	Cys
	50					55					60				
Leu	Val	Ile	Leu	Gln	His	Gln	Ala	Met	Lys	Thr	Pro	Thr	Asn	Tyr	Tyr
	65				70					75					80
Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu	Leu	Gly	Met
				85					90					95	
Pro	Leu	Glu	Val	Tyr	Glu	Met	Trp	Arg	Asn	Tyr	Pro	Phe	Leu	Phe	Gly
			100					105					110		
Pro	Val	Gly	Cys	Tyr	Phe	Lys	Thr	Ala	Leu	Phe	Glu	Thr	Val	Cys	Phe
		115					120					125			
Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg	Tyr	Val	Ala
						135					140				
Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg	Arg	Ala
145					150					155					160
Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu	Phe	Ser	Leu
				165				170						175	
Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	Asn	Gly
			180					185					190		
Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	Pro	Met	Trp

16/28

195	200	205
Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu Leu 210 215 220		
Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg Leu 225 230 235 240		
Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile Gln 245 250 255		
Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu Val Leu 260 265 270		
Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu Phe Phe 275 280 285		
Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val Phe Asn Leu 290 295 300		
Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser Ala Val Asn 305 310 315 320		
Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala Phe Gln 325 330 335		
Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His Asp Pro 340 345 350		
Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys His Phe 355 360 365		
Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys Gln Ser Ser 370 375 380		
Val His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln Met Ser 385 390 395 400		
Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr 405 410		

&lt;210&gt; 9

&lt;211&gt; 1594

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (55)..(942)

&lt;223&gt; IGS4A truncated DNA long version

&lt;400&gt; 9

ggctcagctt gaaacagagc ctcgtaccag gggaggctca ggccttggat ttta atg 57  
Met

17/28

1

tca ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa	105
Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys	
5 10 15	
cta gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg	153
Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu	
20 25 30	
gcc ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct	201
Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser	
35 40 45	
gtg gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg	249
Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu	
50 55 60 65	
gtg tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac	297
Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn	
70 75 80	
tac tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt	345
Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu	
85 90 95	
gga atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg	393
Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu	
100 105 110	
ttc ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg	441
Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val	
115 120 125	
tgc ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac	489
Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr	
130 135 140 145	
gtg gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc	537
Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg	
150 155 160	
cgg gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc	585
Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe	
165 170 175	
tcc ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc	633
Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro	
180 185 190	
aat ggg tcc ctg gtc cca ggt tcg gcc acc tgt acg gtc atc aag ccc	681
Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro	
195 200 205	
atg tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac	729
Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr	



18/28

210	215	220	225	
ctc ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc				777
Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu				
	230	235	240	
aga cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat				825
Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn				
	245	250	255	
att caa aga ccc tgc aga aaa tca gtc aac aag atg ctg tct ttg tgg				873
Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu Trp				
	260	265	270	
agg agt gga gtg aat ccc tgg ctg ctg tgt tca acc tcg tcc atg tgg				921
Arg Ser Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met Trp				
	275	280	285	
tgt cag gtg tct tct tct acc tgagctcagc tgtcaacccc attatctata				972
Cys Gln Val Ser Ser Ser Thr				
290	295			
acctactgtc tcgccgcttc caggcagcat tccagaatgt gatctcttct ttccacaaac				1032
agtggcactc ccagcatgac ccacagttgc cacctgcccac gcggaacatc ttccctgacag				1092
aatgccactt tgtggagctg accgaagata taggtcccca attcccatgt cagtcaccca				1152
tgcacaactc tcacctccca acagccctct ctagtgaaca gatgtcaaga acaaactatc				1212
aaagcttcca ctttaacaaa acctgaattc ttccagagct gactctcctc tatgcctcaa				1272
aacttcagag aggaacatcc cataatgtat gccttctcat atgatattag agaggtagaa				1332
tggctcttac aactcatgta ccattgcta gttttttttt tttaataaac gtgaaaactg				1392
agagttagat ctggtttcaa aaccaagac tgccctgattt ttagttatct ttccactatc				1452
ctaactgcct catgcccctt cactagttca tgccaagaac gtgactggaa aggcattggca				1512
cctatacctt gattaatttc cattaatgga aatgggttcgt cctgagtcac ctacgttccg				1572
agtcaggctg tcactcctac ta				1594

&lt;210&gt; 10

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 10

Met	Ser	Gly	Met	Glu	Lys	Leu	Gln	Asn	Ala	Ser	Trp	Ile	Tyr	Gln	Gln
1				5				10						15	

Lys	Leu	Glu	Asp	Pro	Phe	Gln	Lys	His	Leu	Asn	Ser	Thr	Glu	Glu	Tyr
			20				25						30		

19/28

Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val  
 35 40 45  
 Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val  
 50 55 60  
 Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr  
 65 70 75 80  
 Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu  
 85 90 95  
 Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe  
 100 105 110  
 Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr  
 115 120 125  
 Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg  
 130 135 140  
 Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg  
 145 150 155 160  
 Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu  
 165 170 175  
 Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe  
 180 185 190  
 Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys  
 195 200 205  
 Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe  
 210 215 220  
 Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala  
 225 230 235 240  
 Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala  
 245 250 255  
 Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu  
 260 265 270  
 Trp Arg Ser Gly Val Asn Pro Trp Leu Leu Cys Ser Thr Ser Ser Met  
 275 280 285  
 Trp Cys Gln Val Ser Ser Ser Thr  
 290 295

&lt;210&gt; 11

&lt;211&gt; 1594

20/28

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (64) .. (942)

&lt;223&gt; IGS4A truncated DNA short version

&lt;400&gt; 11

ggctcagctt gaaacagagc ctcgtaccag gggagggtca ggccttggat tttaatgtca 60

ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa cta	108
Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu	
1 5 10 15	

gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc	156
Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala	
20 25 30	

ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct gtg	204
Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val	
35 40 45	

gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg gtg	252
Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val	
50 55 60	

tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac tac	300
Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr	
65 70 75	

tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt gga	348
Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly	
80 85 90 95	

atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg ttc	396
Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe	
100 105 110	

ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg tgc	444
Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys	
115 120 125	

ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac gtg	492
Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val	
130 135 140	

gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc cgg	540
Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg	
145 150 155	

gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc tcc	588
Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser	
160 165 170 175	

ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc aat	636
---	-----

21/28

Leu	Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	Asn	
				180					185					190		
ggg	tcc	ctg	gtc	cca	ggt	tcg	gcc	acc	tgt	acg	gtc	atc	aag	ccc	atg	684
Gly	Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	Pro	Met	
			195					200					205			
tgg	atc	tac	aat	ttc	atc	atc	cag	gtc	acc	tcc	ttc	cta	ttc	tac	ctc	732
Trp	Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	Tyr	Leu	
		210					215					220				
ctc	ccc	atg	act	gtc	atc	agt	gtc	ctc	tac	tac	ctc	atg	gca	ctc	aga	780
Leu	Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	Arg	
	225					230					235					
cta	aag	aaa	gac	aaa	tct	ctt	gag	gca	gat	gaa	ggg	aat	gca	aat	att	828
Leu	Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala	Asn	Ile	
240					245				250					255		
caa	aga	ccc	tgc	aga	aaa	tca	gtc	aac	aag	atg	ctg	tct	ttg	tgg	agg	876
Gln	Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Ser	Leu	Trp	Arg	
				260				265					270			
agt	gga	gtg	aat	ccc	tgg	ctg	ctg	tgt	tca	acc	tcg	tcc	atg	tgg	tgt	924
Ser	Gly	Val	Asn	Pro	Trp	Leu	Leu	Cys	Ser	Thr	Ser	Ser	Met	Trp	Cys	
			275				280						285			
cag	gtg	tct	tct	tct	acc	tgagctcagc	tgtcaacccc	attatctata								972
Gln	Val	Ser	Ser	Ser	Thr											
			290													
acctactgtc	tcgccgcttc	caggcagcat	tccagaatgt	gatctcttct	ttccacaaac											1032
agtggcactc	ccagcatgac	ccacagttgc	cacctgccca	gcggaacatc	ttcctgacag											1092
aatgccactt	tgtggagctg	accgaagata	taggtcccca	attcccatgt	cagtcattcca											1152
tgcacaactc	tcacctccca	acagccctct	ctagtgaaca	gatgtcaaga	acaaactatc											1212
aaagcttcca	ctttaacaaa	acctgaattc	tttcagagct	gactctcctc	tatgcctcaa											1272
aacttcagag	aggaacatcc	cataatgtat	gccttctcat	atgatattag	agaggtagaa											1332
tggctcttac	aactcatgta	cccattgcta	gttttttttt	tttaataaac	gtgaaaactg											1392
agagttagat	ctgggtttcaa	aaccaagac	tgectgattt	ttagttatct	ttccactatc											1452
ctaactgcct	catgcccctt	cactagttca	tgccaagaac	gtgactggaa	aggcatggca											1512
cctatacctt	gattaatttc	cattaatgga	aatggttcgt	cctgagtcac	ctacgttccg											1572
agtcaggctg	tcactcctac	ta														1594

&lt;210&gt; 12

&lt;211&gt; 293

22/28

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

Met	Glu	Lys	Leu	Gln	Asn	Ala	Ser	Trp	Ile	Tyr	Gln	Gln	Lys	Leu	Glu	1	5	10	15
Asp	Pro	Phe	Gln	Lys	His	Leu	Asn	Ser	Thr	Glu	Glu	Tyr	Leu	Ala	Phe	20	25	30	
Leu	Cys	Gly	Pro	Arg	Arg	Ser	His	Phe	Phe	Leu	Pro	Val	Ser	Val	Val	35	40	45	
Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val	Leu	Val	Cys	50	55	60	
Leu	Val	Ile	Leu	Gln	His	Gln	Ala	Met	Lys	Thr	Pro	Thr	Asn	Tyr	Tyr	65	70	75	80
Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu	Leu	Gly	Met	85	90	95	
Pro	Leu	Glu	Val	Tyr	Glu	Met	Trp	Arg	Asn	Tyr	Pro	Phe	Leu	Phe	Gly	100	105	110	
Pro	Val	Gly	Cys	Tyr	Phe	Lys	Thr	Ala	Leu	Phe	Glu	Thr	Val	Cys	Phe	115	120	125	
Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg	Tyr	Val	Ala	130	135	140	
Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg	Arg	Ala	145	150	155	160
Leu	Arg	Ile	Leu	Gly	Ile	Val	Trp	Gly	Phe	Ser	Val	Leu	Phe	Ser	Leu	165	170	175	
Pro	Asn	Thr	Ser	Ile	His	Gly	Ile	Lys	Phe	His	Tyr	Phe	Pro	Asn	Gly	180	185	190	
Ser	Leu	Val	Pro	Gly	Ser	Ala	Thr	Cys	Thr	Val	Ile	Lys	Pro	Met	Trp	195	200	205	
Ile	Tyr	Asn	Phe	Ile	Ile	Gln	Val	Thr	Ser	Phe	Leu	Phe	Tyr	Leu	Leu	210	215	220	
Pro	Met	Thr	Val	Ile	Ser	Val	Leu	Tyr	Tyr	Leu	Met	Ala	Leu	Arg	Leu	225	230	235	240
Lys	Lys	Asp	Lys	Ser	Leu	Glu	Ala	Asp	Glu	Gly	Asn	Ala	Asn	Ile	Gln	245	250	255	
Arg	Pro	Cys	Arg	Lys	Ser	Val	Asn	Lys	Met	Leu	Ser	Leu	Trp	Arg	Ser	260	265	270	
Gly	Val	Asn	Pro	Trp	Leu	Leu	Cys	Ser	Thr	Ser	Ser	Met	Trp	Cys	Gln				

23/28

275

280

285

Val Ser Ser Ser Thr  
290

<210> 13  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Degenerated  
primers

<220>  
<221> variation  
<222> (21)  
<223> A,C,G or T

<220>  
<221> variation  
<222> (24)  
<223> A, C, G or T

<400> 13  
ctcatcttcg cggtgggcrc ngynngg

26

<210> 14  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Degenerated  
primers

<220>  
<221> variation  
<222> (22)  
<223> C or Inosine

<220>  
<221> variation  
<222> (25)  
<223> A, C, G or T

<220>  
<221> variation  
<222> (28)  
<223> A, C, G or T

<400> 14  
ggccaggcag cgctccgcgc tnarncyngc d

31

24/28

<210> 15  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Degenerated  
primers

<400> 15  
gaartartag ccrcgrcagc cw

22

<210> 16  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 16  
ccatcctaatacgcactcact atagggc

27

<210> 17  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 17  
actcactata gggctcgagc ggc

23

<210> 18  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 18  
ggatcccaaa taagaaagg tagttgc

27

<210> 19  
<211> 29  
<212> DNA  
<213> Artificial Sequence

25/28

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 19

aaagggtagt tgcgccacat ctcataagac

29

&lt;210&gt; 20

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 20

aggtctatga gatgtggcgc aactaccct

29

&lt;210&gt; 21

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 21

atgtggcgc actacccttt cttatttggg

30

&lt;210&gt; 22

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Degenerated  
primers

&lt;400&gt; 22

cggaagttgg cggacacgrv rttrta

26

&lt;210&gt; 23

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 23

gctcagcttg aaacagagcc tcgtacc

27



26/28

<210> 24  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 24  
ccatgtggat ctacaatttc atcatcc

27

<210> 25  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 25  
aagacaaatc tcttgaggca gatgaaggg

29

<210> 26  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 26  
gatgctgttt gtcttggtct tagtgtttgc

30

<210> 27  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 27  
ggatgatgaa attgtagatc cacatgggc

29

<210> 28  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

27/28

<400> 28  
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<210> 29  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 29  
tagtaggagt gacagcctga ctcggaacg 29

<210> 30  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 30  
aacgtagatg actcaggacg aaccatttcc 30

<210> 31  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 31  
tcgtaccagg ggaggctcag gc 22

<210> 32  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 32  
cctcttcagc ctggcggtct ctg 23

<210> 33  
<211> 22  
<212> DNA  
<213> Artificial Sequence

28/28

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 33

ggaggcgaag cacacggtct ca

22

&lt;210&gt; 34

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; (1)

&lt;223&gt; Labeled with 6-carboxyfluorescein

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; (34)

<223> Labeled with  
N,N,N',N'-tetramethyl-6-carboxyrhodamin

&lt;400&gt; 34

agatgtggcg caactaccct ttcttggtcg ggcc

34